STIC-Biotech/ChemLib

From: Sent:

Ibrahim, Medina A. Tuesday, May 27, 2003 7:21 AM STIC-Biotech/ChemLib

To: Subject:

09/977, 137

(STIC)

Please search the following:

1. SEQ ID NO:3-4.

2. oligo search of SEQ ID NO:3-4.

Please search both commercial and patent databases (including pending). Thanks

Medina A. Ibrahim Patent Examiner GAU:1638 CM1-9E03 mailbox-9E12 (703)306-5822

Searcher:_____ Phone: Location:____ Date Picked Up: 5 PK
Date Completed: 4 Searcher Prep/Review: 1 Clerical:_ Online time:_____

TYPE OF SEARCH: NA Sequences:_____ AA Sequences:_____ Structures:_____ Bibliographic:_____ Litigation: Full text: Patent Family:_____ Other:_____

VENDOR/COST (where applic.) STN:_____ DIALOG:____ Questel/Orbit:_____ DRLink:_____ Lexis/Nexis:_____ Sequence Sys.:_______
WWW/Internet:_____ Other (specify):_____

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1 atgacacactgcgaggaggc.....agggggaatgtttcctgcccg 321
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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18 18	18	19	19	Score
5. 66	5.6	5.9	5.9	Query Match
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ALIGNMENTS

FEATURES source		TITLE JOURNAL COMMENT		ACCESSION VERSION KEYWORDS SOURCE	RESULT 1 C91774/c LOCUS DEFINITION
POLYA=NO. Location/Qualifiers 1. 305 /organism="Oryza sativa (japonica cultivar-group)"	NICE GENOME RESEARCH FLOGIUM, NAMES 1905-8602, Japan 305-8602, Japan Tel: 81-298-38-7441 Fax: 81-298-38-7468 Email: tsasaki@abr.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/ PROJECT = 'RGP'	Rice cDNA from panicle Rice cDNA from panicle Unpublished (1997) Contact: Takuji Sasaki Contact: T	Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Seraki, T. and Vamamoto, K.	C91774. C91774.1 GI:3061142 C91774.1 GI:3061142 Oryza sativa (japonica cultivar-group). Oryza sativa (japonica cultivar-group)	C91774 305 bp mRNA linear EST 04-APR-2002 C91774 Rice panicle shorter than 3cm Oryza sativa (japonica cultivar-croup) cDNA clone E31517 lA, mRNA sequence.

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 BE791590 1099 bp mRNA linear EST 20-9 601585915F1 NIH_MGC_7 Homo sapiens cDNA clone IMAGE:3940395
mRNA sequence
                                                                                                                                                                                        19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Unpublished (2001)
Contact: O'Connell, MA
Department of Agronomy and Horticulture
New Mexico State University
MSC 30, P.O. Box 30003, Las Cruces, NM 88003, USA
Tel: 505 646 5172
Fax: 505 646 6041
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Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Capsicum. 1 (bases 1 to 777)
Nevarez,J.G. and O'Connell,M.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       B1480603 777 bp mRNA linear EST 28-EST0056 Habanero leaf cDNA Capsicum chinense cDNA clone Jn similar to Cationic Peroxidase, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Seq primer: T3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: moconnel@nmsu.edu
Insert Length: 1200 Std
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Capsicum chinense.
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                                                                                                                                                                                                                                                                                                                  /clone_lib="Habanero leaf cDNA"
/dev_stage="drought-stressed"
                                                                                                                                                                                                                                                                                                                                                         /organism="Capsicum chinense"
/cultivar="Early Scotch Bonnet"
/db_xref="taxon:80379"
/clone="Jn 51"
                                                                                                                                                                                                                                                                              /note="Organ: leaf; Vector: Uni-zap xr; Site_1: EcoR1;
Site_2: xho 1"
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110 c 92 g
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/db_xref="taxon:39947"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                            963 GGGATCCTCAGGCACCCAC 981
  Tumor Gene Index
Unpublished (1997)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Christopher A. Moskaluk, M.D., Ph.D., Michael
                                                                                                                                                                                                                                                                                                                 A1824830 344 bp mRNA linear EST 16-DEC-1999 wb02d07.x1 NCI_CGAP_GC6 Homo sapiens cDNA clone IMAGE:2304493 3' similar to SW:HMG2_CHICK P26584 HIGH MOBILITY.GROUP PROTEIN HMG2 ;,
                                                                                                      NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Euthoria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 344)
                                                                                                                                                                                                               Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        19;
                                                                                                                                                                                                                                                                   AI824830.1 GI:5445501
                                                                                                                                                                                                                                                                                                       mRNA sequence.
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Tissue Procurement: DCTD/DTp
CDNA Library Preparation: Ling Hong/Rubin Laboratory
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at: image.llnl.gov
Plate: LLCM790 row: m column: 04
High quality sequence start: 7
High quality sequence start: 7
LCCATION/Qualifiers
1 1000
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National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

[ (bases 1 to 1099)
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Emumert-Buck, M.D.,
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/tissue_type="small cell carcinoma"
/cell_line="MGC3"
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/db_xref="taxon:9606"
/cione="IMAGE:3940395"
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100.0%; Pred. No.
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CDNA Library Arrayed by: Washington University Genome Sequencing Center
DNA Sequencing by: Washington University Genome Sequencing Center
Clone distribution: NCI-CGAP clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
www-bio.llnl.gov/bbrp/image/image.html
Insert Length: 653 Std Error: 0.00
Seq primer: -40UP from Gibco
High quality sequence stop: 264.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                              McDermott, J.P., Silflow, C., Stern, D. and Surzycki, R. Analyses of the Chlamydomonas reinhardtii Genome: A Model, Unicellular System for Analyzing Gene Function and Regulation in Vascular Plants; project phase 2 Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             894030809.x3 C. reinhardtii CC-1690, normalized, Lambda Chlamydomonas reinhardtii cDNA, mRNA sequence.
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Eukaryota; Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Grossman, A., Davies, J., Federspiel, N., Harris, E., Lefebvre, P.,
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                                                                                                                                                                                                                             Tel: 919 613 8164
Fax: 919 613 8177
                                                                                                                                                                                                                                                                                                                                                                Contact: Elizabeth H. Harris
                                                                                                                                                                                                                                                                                     Durham, NC 27708-1000, USA
                                                                                                                                                                                                                                                                                                              Duke University
                                                                                                                                                                                                                                                                                                                                       DCMB Box 91000
                                                                                                                                                                                                            Email: chlamy@duke.edu
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone="IMAGE:2304493"
/clone_lib="NCI_CGAP_GC6"
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/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /tissue_type="pooled germ cell tumors"
/lab_host="DH10B"
                      /organism="Chlamydomonas reinhardtii"
/strain="CC-1690 wild type mt+ 21gr"
/db_xref="taxon:3055"
/clone_lib="C. reinhardtii CC-1690, normalized, Lambda Zap
II"
/note="Vector: pBluescript II SK-; Site_1: EcoRI; Site_2:
                                                                                                                                                                          Location/Qualifiers
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; Pred. No. 1.5e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: cgapbs-remail.nih.gov
This clone is available royalty-free through LLNL; contact the
IMAGE Consortium (info@image.llnl.gov) for further information.
Seq primer: -400P from Gibco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 398)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCI CGAP http://www.ncbi.nlm.nih.gov/ncicgap.
National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Tumor Gene Index
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 High quality sequence stop: 392.
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/clone_lib="Soares_NFL_T_GBC_S1"
                                                                                                                                                                                                                                                                                                                                                                 /clone="IMAGE:2974523"
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BM487398
425 bp mRNA linear EST 07-FEB-200: pgm2n.pk004.hl Normalized Chicken Breast Muscle, Leg Muscle, and Epiphyseal Growth Plate CDNA library (pgm2n) Gallus gallus CDNA Clone pgm2n.pk004.hl 5' similar to gb|AAK15544.1 (AF346565) signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?t1-&t2-RC6-GN0070-120
900-022-E10&t3-2000-09-12&t4-1)
Seq primer: puc 18 forward
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Dias Neto,E., Garcia Correa,R., Verjovski-Almeida,S., Briones,M.R.,
Nagai,M.A., Bordin,S., Costa,F.F.,
Goldman,G.H., Carvalho,A.F., Matsukuma,A., Baia,G.S., Simpson,D.H.,
Brunstein,A., deOliveira,P.S., Bucher,P., Jongeneel,C.V., O'Hare
,M.J., Soares,F., Brentani,R.R., Reis,L.F., de Souza,S.J. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Laboratory of Cancer Genetics
Ludwig Institute for Cancer Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Shotgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Simpson A.J.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                                                                                                                            /note="Organ: placenta_normal; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and cDNA amplification were performed under low stringency conditions."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /dev_stage="Adult"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone_lib="GN0070"
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1 (bases 1 to 425)
Porter,T.E. and Cogburn,L.A.
ESTS from Normalized Chicken Pituitary/Hypothalamus/Pineal cDNA
library, USDA/IFARS Animal Genome Project
Unpublished (2002)
                                                                                                                                                                                                                                                                                                            BM491850
425 bp mRNA linear EST 07-FEB-200: pgp2n.pk007.j9 Normalized Chicken Pituitary/Hypothalamus/Pineal Library (pgp2n) Gallus gallus cDNA clone pgp2n.pk007.j9 5' similar to gb|AAK15544.1 (AF346565) signal sequence receptor beta subunit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          86 GGAGGCCAGCAGCCTGGC 69
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                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianidae; Galliformes; Calliformes; Phasianidae;
                                                                                                                                                                                         Gallus gallus
                                                                                                                                                                                                                     chicken
                                                                                                                                                                                                                                                         BM491850.1 GI:18612781
                                                                                                                                                                                                                                                                                      [Xenopus laevis], mRNA sequence. BM491850
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
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Tel: 302-831-1335
Fax: 302-831-2822
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Contact: Larry A. Cogburn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: cogburn@udel.edu,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         University of Delaware
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sequence receptor beta subunit [Xenopus laevis], mRNA sequence. BM487398
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="Vector: pcMvSpORT6; Library made from equivalent pools of total RNA isolated from each tissue (embryonic muscle 33.3%; juvenile muscle 33.3%; and epiphyseal growth plate 33.3% of the final RNA pool). Single pass sequencing from 5'-end"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /dev_stage="Breast,leg:Embryo(d19);post-hatch(ld,1,3,5,7,9,11 weeks);growth plate(ld,7d,14d post-hatch)"
/lab_host="E. coli_EMDH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /tissue_type="Breast muscle, leg muscle and epiphyseal
growth plate"
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/clone_lib="Normalized Chicken Breast Muscle, Leg Muscle, and Epiphyseal Growth Plate cDNA library (pgm2n)"
/sex="Male and Female"
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Strains 90 & 21"
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nes 0;
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Location/Qualifiers
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Fax: 302-831-2822
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                                                                                                                                                                                                                                                                                                                                                                                                                                           Molecular Endocrinology
University of Delaware
40 Townsend Hall, Newark, DE 19717, USA
Tel: 302 831-1345
Fax: 302-831-3411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gallus gallus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Burnside, J., Morgan, R.W. and Cogburn, L.A. Chicken ESTs from a normalized liver library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Unpublished (2001)
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/tissue_type="Pituitary Gland/Hypothalamus/Pineal Gland"
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/clone_lib="Normalized Chicken
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           /note="Vector: pCMVSPORT 6" 122 c 134 g 113 t
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/clone="pglln.pk001.d18"
/clone_lib="Normalized Liver Library"
/clone_lib="Normalized Liver Library"
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                                                                          /tissue_type="liver"
/lab_host="E.coli EMDH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ze71g07.s1 Soares_fetal_heart_NDHH19W Homo sapiens cDNA clone IMAGE:364476 3', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                This clone is available royalty-free through LLNL; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 527 Std Error: 0.00 Seq primer: -40M13 fwd. from Amersham High quality sequence stop: 67.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108
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Fax: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Washington University School of Medicine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Wilson RK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: est@watson.wustl.edu
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                                                                                                                                                                                                                                                                                                                                              double-stranded CDNA was size selected, ligated to Eco RI adapters (Pharmacia), digested with Not I and cloned into the Not I and Eco RI sites of a modified pT773 vector (Pharmacia). Library went through one round of normalization to a Cot = 5. Library constructed by M.Fatima Bonaldo. This library was constructed from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /lab_host="DH10B (ampicillin resistant)"
/note="Organ: heart; Vector: pT7T3D (Pharmacia) with a /note="Organ: heart; Vector: pT7T3D (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; 1st strand cDNA was primed with a Not I - oligo(dT) primer [5', strand cDNA was primed with a Not I - oligo(dT) primer [5', strand cDNA was primed with a Not I - oligo(dT) primer [5', strand cDNA was primed with a Not I - oligo(dT) primer [5', strand cDNA was primed with a Not I - oligo(dT) primer [5', strand cDNA was primed with a Not I - oligo(dT) primer [5', strand cDNA was primed with a Not I - oligo(dT) primer [5', strand cDNA was primed with a Not I - oligo(dT) primer [5', strand cDNA was primed with a Not I - oligo(dT) primer [5', strand cDNA was primed with a Not I - oligo(dT) primer [5', strand cDNA was primed with a Not I - oligo(dT) primer [5', strand cDNA was primed with a Not I - oligo(dT) primer [5', strand cDNA was primed with a Not I - oligo(dT) primer [5', strand cDNA was primed with a Not I - oligo(dT) primer [5', strand cDNA was primed with a Not I - oligo(dT) primer [5', strand cDNA was primed with a Not I - oligo(dT) primer [5', strand cDNA was primed with a Not I - oligo(dT) primer [5', strand cDNA was primed with a Not I - oligo(dT) primer [5', strand cDNA was primed with a Not I - oligo(dT) primer [5', strand cDNA was primed with a Not I - oligo(dT) primer [5', strand cDNA was primed with a Not I - oligo(dT) primer [5', strand cDNA was primed with a Not I - oligo(dT) primer [5', strand cDNA was primed with a Not I - oligo(dT) primer [5', strand cDNA was primed with a Not I - oligo(dT) primer [5', strand cDNA was primed with a Not I - oligo(dT) primer [5', strand cDNA was primed with a Not I - oligo(dT) primer [5', strand cDNA was primed with a Not I - oligo(dT) primer [5', strand cDNA was primed with a Not I - oligo(dT) primer [5', strand cDNA was primed with a Not I - oligo(dT) primer [5', strand cDNA was primed with a Not I - oligo(dT) primer [5', strand cDNA was primed with a Not I - o
                                                                                                                                                                                                                                      same fetus as the fetal lung library, Soares fetal lung NbHL19M."
75 c 98 g 132 t 3 others
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/db_xref="taxon:9606"
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100.0%;
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                                                                                                                         5.6%;
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                                                                                       Score 18; DB 9; L; Pred. No. 1.6e+02;
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                                                                                                                         DB 9;
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                                                                                                                                 Length 460;
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           Cogburn, L.A. and Monsonego-Ornan, E. ESTs from Normalized Chicken Breast
                                                                                                                Gallus gallus
                                                                                                                                                                                      pgm2n.pk002.cl Normalized Chicken Breast Muscle, Leg Muscle, and Epiphyseal Growth Plate cDNA library (pgm2n) Gallus gallus cDNA clone pgm2n.pk002.cl 5' similar to gblAAK15544.1 (AF346565) signal sequence receptor beta subunit [Xenopus laevis], mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                               18;
                                                       Archosauria; Aves; Neognathae; Phasianinae; Gallus.
                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Archosauria; Aves; Neognathae; Galliformes; Phasiani
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                                                                                                                                    chicken.
                                                                                                                                                                       BM486606.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Joan Burnside
Molecular Endocrinology
University of Delaware
40 Townsend Hall, Newark, DE 19717,
Tel: 302 831-1345
Fax: 302-831-3411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 (bases 1 to 467)
Burnside, J., Morgan, R.W. and Cogburn, L.A.
Chicken ESTS from a normalized liver library
Unpublished (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                p911n.pk015.n15 Normalized Liver Library Gallus gallus cDNA clone p911n.pk015.n15 5 similar to sp1p23438 |SSRB, CANEA TRANSLOCOM-ASSOCIATED PROTEIN, BETA SUBUNIT PRECURSOR (TRAP-BETA) (SIGNAL SEQUENCE RECEPTOR BETA SUBUNIT) (SSR-BETA) (GP25H) pir|A33679 signal sequence receptor beta chain precursor dog,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: joan@UDel.Edu, www.chickest.udel.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            chicken.
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                                         (bases 1 to 490)
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from Normalized Chicken Breast Muscle,
                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /tissue_type="liver"
/lab_host="E.coli EMDH10B"
/note="Vector: pCMVSPORT 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Gallus gallus"
/db_xref="taxon:9031"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone_lib="Normalized Liver Library"
/sex="Male and Female"
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                                                                                         Euteleostomi;
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        This sequence was derived f
Project. This entry can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  86
                     Email: asimpson@ludwig.org.br
This sequence was derived from the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15 GGAGGCCAGCAGCCTGGC 32
                                                                            Fax: +55-11-2707001
                                                                                              Tel: +55-11-2704922
                                                                                                                                                       Laboratory of Cancer Genetics Ludwig Institute for Cancer Research
                                                                                                                                                                                                 Contact: Simpson A.J.G.
                                                                                                                                                                                                                                                                           Shotgun sequencing of the human transcriptome with ORF expressed
                                                                                                                                     Rua Prof. Antonio Prudente 109,
                                                                                                                                                                                                                             20202663
                                                                                                                                                                                                                                                                  sequence tags
                                                                                                                                                                                                                                                                                                                                                                                         1 (bases 1 to 495)
Dias Neto, E., Garcia Correa, R., Verjovski-Almeida, S., Briones, M.R.,
                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BF850925 495 bp mRNA linear MR4-EN0075-241100-001-f07 EN0075 Homo sapiens cDNA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
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Fax: 302-831-2822
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note-"Vector: pCMVSPORT6; Library made from equivalent pools of total RNA isolated from each tissue (embryonic muscle 33.3%; juvenile muscle 33.3%; and epiphyseal growth plate 33.3% of the final RNA pool). Single pass sequencing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 from 5'-end"
132 c
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/clone_lib="Normalized Chicken Breast Muscle, Le
/clone_lib="Normalized Chicken Breast Muscle, Le
/clone="pgm2n.pk002.c1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /tissue_type="Breast muscle, leg muscle and epiphyseal
growth plate"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /dev_stage="Breast,leg:Embryo(d19);post-hatch(1d,1,3,5,7,9
,11 weeks);growth plate(1d,7d,14d post-hatch)"
//lab_host="E. coli EMDH10B"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="taxon:9031"
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             seen
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FAPESP/LICR Human Cancer Genome the following URL
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RESULT 15
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                    Program for Rat Gene Discovery and Mapping
University of Iowa
451 Eckstein Medical
Research Building Iowa City, IA 52242, USA
Tel: 319 335 8250
Fax: 319 335 9565
Email: msoares@blue.weeg.uiowa.edu
cDNA Library Preparation: M.B. Soares Lab Clone distribution:
clones will be available through Research Genetics (www.resgen.com)
This clone is also available through the I.M.A.G.E. Consortium at
LLNL (info@image.llnl.gov), INAGE ID- 1774925
Seq primer: M.3 Forward.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BF550791 512 bp mRNA linear EST 12-DH UI-R-CO-jp-e-05-0-UI.rl UI-R-CO Rattus norvegicus cDNA clone UI-R-CO-jp-e-05-0-UI 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Métazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rattus norvegicus
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241100-001-f07&t3=2000-11-24&t4=1)
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/dev_stage="Adult"
/dev_stage="adult"
/lab host="DH10B (Life Technologies)"
/lab host="DH10B (Life Technologies)"
/note="Vector: pT73D-Pac (Pharmacia) with a modified polylinker; Site_1: Not I; Site_2: Eco RI; The UI-R-C0 library is a subtracted library derived from the UI-R-Al
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/db_xref="taxon:9606"
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                                                                                                                                                          /strain="Sprague-Dawley"
/db_xref="taxon:10116"
/clone="UI-R-C0-jp-e-05-0-UI"
                                                                                                                                  /clone_lib="UI-R-CO"
                                                                                                                                                                                                                                    /organism="Rattus norvegicus"
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Pred. No.
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SOURCE

COMMENT

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ORIGIN

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Local Similarity 100.0%;
13 GAGGAGGCCAGCCTG
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                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        and UI-R-El libraries. The UI-R-Al library consisted of a mixture of individually tagged normalized libraries constructed from rat placenta, adult lung, brain, liver, kidney, heart, spleen, ovary, and muscle. The UI-R-El library consisted of a mixture of individually tagged normalized libraries constructed from 8, 12 and 18-day embryo. The tag is a string of 3-5 nucleotides present between the Not I site and the oligo-dT track which allows identification of the library of origin of a clone within the mixture. The subtracted library (UI-R-CO) was constructed as follows: PCR amplified CDNA inserts from a pool of UI-R-Al and UI-R-El clones from which 3' ESTs had been derived was used as a driver in a hybridization with the pooled UI-R-Al and UI-R-El library in the form of single-stranded circles. The remaining single-stranded circles (subtracted library) was purified by hydroxyapatite column chromatography, converted to double-stranded circles and electroporated into DH10B bacteria (Life Technologies) to generate the UI-R-CO library. This procedure has been previously described. PROMED ALL TERMS AND ALL TERM
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                                                                                                   Mismatches
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hes 0;
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Job time : 1516 secs Search completed: June 2, 2003, 09:04:39 밁 δõ

378 GAGGAGGCCAGCAGCCTG

395

ORIGIN

Matches Query Match Best

BASE COUNT

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Minimum
Maximum
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Perfect score:
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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1: /cgn2-6/ptodata/1/
2: /cgn2-6/ptodata/1/
3: /cgn2-6/ptodata/1/
4: /cgn2-6/ptodata/1/
5: /cgn2-6/ptodata/1/
6: /cgn2-6/ptodata/1/
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                                                          /cgn2_6/ptodata/1/ina/5A_COMB.seq:*
/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
/cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*
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4 US-09-103-840A-2
4 US-09-103-840A-1
US-08-675-508-10
US-08-675-508-10
US-08-675-508-10
US-08-675-508-11
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US-08-465-380-115
US-08-486-399-115
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2140.070 Million cell updates/sec
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  Sequence 2, Appli Sequence 13, Appli Sequence 10, Appli Sequence 10, Appli Sequence 11, Appli Sequence 115, Appli Sequence 1115, Appli Sequence 1115, Appli Sequence 1116, Appli Sequence 1117, Appli Sequence 27, Appli Sequence 28, Appli Sequence 29, Ap
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NUMBER OF SEQ ID NOS: 2

RESULT 2 US-09-103-840A-1 ; Sequence 1, Application US/09103840A ; Sequence 1, Application US/09103840A ; Patent No. 6294328 ; Patent No. 6294328 ; Patent INFORMATION: ; APPLICANT: FLEISCHMAN, Robert D. ; APPLICANT: WHITE, Owen R. ; APPLICANT: VENTER, John C. ; APPLICANT: VENTER, John C. ; TITLE OF INVENTION: DANA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBAC ; TITLE OF INVENTION: TUBERCULOSIS ; FILE REFERENCE: 24366-20007.00 ; CURRENT APPLICATION NUMBER: US/09/103,840A ; CURRENT FILLING DATE: 1998-06-24 ; NUMBER OF SEQ ID NOS: 2	Qy 66 GGCCGACTTGGCGCGCA 82	Query Match 5.3%; Score 17; DB 4; Length 4403765; Best Local Similarity 100.0%; Pred. No. 4.4; Matches 17; Conservative 0; Mismatches 0; Indels 0;	PEATURE: "JONG COLOR PEATURE: PEATURE: PEATURE: OTHER INFORMATION: "n" bases at various positions throughout OTHER INFORMATION: "n" bases at various positions throughout OTHER INFORMATION: represent a, t, c or g (S-09-103-840A-2	LENGTH: 44 TYPE: DNA	ULT 1 09-103-840A-2 equence 2, Application US/09103840A atent No. 6294328 atent No. 6294328 applicanT: FLEISCHMAN, Robert D. APPLICANT: FRASE, Claire M. APPLICANT: FRASE, Claire M. APPLICANT: VENTER, John C. TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS TITLE OF INVENTION: TUBERCULOSIS FILE REFERENCE: 24366-20007.00 CURRENT APPLICATION NUMBER: US/09/103,840A CURRENT FALING DATE: 1998-06-24 NUMBER OF SEQ ID NOS: 2 NUMBER OF SEQ ID NOS: 2 SOSTWARE: Patentin Ver. 2.1	ALIGNMENTS	28 15 4.7 60 2 US-08-480-397-112 Sequence 30 15 4.7 60 2 US-08-486-397-113 Sequence 31 15 4.7 60 2 US-08-486-397-113 Sequence 31 15 4.7 60 2 US-08-486-397-114 Sequence 31 15 4.7 60 2 US-08-486-399-112 Sequence 32 15 4.7 60 2 US-08-486-399-113 Sequence 33 15 4.7 60 2 US-08-486-399-113 Sequence 34 15 4.7 60 2 US-08-486-399-114 Sequence 35 15 4.7 60 2 US-08-481-965-113 Sequence 36 15 4.7 60 2 US-08-461-965-114 Sequence 37 15 4.7 60 2 US-08-461-965-114 Sequence 38 15 4.7 60 2 US-08-326-110A-28 Sequence 41 15 4.7 60 2 US-08-326-110A-29 Sequence 41 15 4.7 60 2 US-08-634-641-113 Sequence 41 15 4.7 60 2 US-08-634-641-114 Sequence 41 15 4.7 60 2 US-08-634-641-114 Sequence 51 4.7 60 2 US-08-634-641-114 Sequence 51 4.7 60 3 US-09-249-471-113 Sequence 51 51 51 51 51 51 51 51 51 51 51 51 51
MYCOBACTERIUM		403765 s 0	hout the sequence		IN MYCOBACTERIUM		Sequence 29, Appl Sequence 112, App Sequence 113, App Sequence 114, App Sequence 114, App Sequence 113, App Sequence 114, App Sequence 114, App Sequence 114, App Sequence 27, Appl Sequence 28, Appl Sequence 29, Appl Sequence 112, App Sequence 113, App Sequence 113, App Sequence 114, App Sequence 114, App Sequence 114, App Sequence 117, App

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RESULT 4
US-08-675-508-10/c
; Sequence 10, Application US/08675508
; Patent No. 5856136
; Patent No. 5856136
                                                                                                                                                                                                                                                 US-08-675-508-13
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                                                                                                                                                                                                                Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: FASTSEQ VERSION 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: U708/675,50
FILLING DATE: Filed Herewith
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0060
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
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                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION FOR SEQ ID NO:
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ORGANISM: Mycobacterium tuberculosis
OTHER INFORMATION: H37Rv
                                                                                                                                                                                                                                                                         IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
LENGTH: 261 base pairs
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MEDIUM TYPE: Diskett
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NUMBER OF SEQUENCES:
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CITY: Palo Alto
STATE: CA
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                                                                                                                                                                        y Match 5.0%; Score 16; DB 2; Length 261; Local Similarity 100.0%; Pred. No. 21; hes 16; Conservative 0; Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                              linear
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100.0%; Pred. No. 4.4;
ative 0; Mismatches
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                                                                                                                                                                                                                                                                                     Sequence 16, Application US/08675508
Patent NO. 5856136
GENERAL INFORMATION:
APPLICANT: AU-YOUNG, Janice
TITLE OF INVENTION: NOVEL HUMAN STEM CELL ANTIGENS
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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INFORMATION FOR SEQ ID NO:
                                OPERATING SYSTEM: DOS
SOFTWARE: FRS45EQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/675,508
FILING DATE: Filed Herewith
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
                                                                                                                                                                  COUNTRY: U.S.
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IMMEDIATE SOURCE:
LIBRARY: BRSTT
CLONE: 604702
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855.0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: Filed Herew ATTORNEY/AGENT INFORMATION: NAME: Billings, Lucy J.
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TITLE OF INVENTION: NOVEL HUMAN STEM CELL ANTIGENS
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
            NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
                                                                                                                                                                                                                                                      STREET: 3174 POR
CITY: Palo Alto
REFERENCE/DOCKET NUMBER: PF-0066 US
                                                                                                                                                       COMPUTER:
                                                                                                                                                                                                                                             STATE:
                                                                                                                                                                                                                                                        ADDRESSEE: Incylo---
ADDRESSEE: 3174 Porter Drive
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CITY: Palo Alto
STATE: CA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: UZIP: 94304
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                h 5.0%; Score 16; DB 2;
Similarity 100.0%; Pred. No. 21;
16; Conservative 0; Mismatches
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                                                                                                                                                   IBM Compatible
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SYSTEM: DOS
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US-08-675-508-16
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US-08-675-508-9/c
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                                                                                                                  US-08-675-508-9
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                                                            Matches
                                                                                     Query Match
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INFORMATION FOR SEQ ID NO: 9:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Au-Young, Janice
TITLE OF INVENTION: NOVEL HUMAN STEM CELL ANTIGENS
NUMBER OF SEQUENCES: 26
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/675
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 94304
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: PF
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
                                                                                                                                                                                                                                                                                                                                             FILING DATE: Filed Herewith ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LIBRARY: Duant
                                                                                                                                                                IMMEDIATE SOURCE:
                                                                                                                                                                              MOLECULE TYPE:
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Local Similarity 100.0%; Pred. No. 21;
hes 16; Conservative 0; Mismatches
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CITY: Palo Alto
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                                                                                                                                   CLONE:
                                                                                                                                                LIBRARY:
                                                                       Local Similarity
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 27 CCAGCAGCCTGGCCGA 12
                              20 CCAGCAGCCTGGCCGA 35
                                                          16; Conservative
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nucleic acid
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                                                            0; Mismatches
                                                                            Score 16;
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; Sequence 11, Application US/08675508
; Patent No. 5856136
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US-08-675-508-11/c
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US-08-675-508-12/c
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                       GENERAL INFORMATION:
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TITLE OF INVENTION: NOVEL HUMAN STEM CELL ANTIGENS
NUMBER OF SEQUENCES: 26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/675,508
FILING DATE: Filed Herewith
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0066 US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 289 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE:
                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                        TITLE OF INVENTION: NO NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
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                                                                              COUNTRY:
                                                                                                                      STREET: 3174 FOR CITY: Palo Alto
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                                                                                                                                                                                                                                                                                                                                                                                                                                       Local Similarity 100.0%;
               COMPUTER: IBM CON OPERATING SYSTEM:
                                                                                                              STATE:
SOFTWARE:
                                                                                                                                                            ADDRESSEE:
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                                                                               94304
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3174 Porter Drive
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                                                                                             U.S.
                                                                                                                                                                                                                       Au-Young, Janice
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FastSEQ Version 1.5
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                                                                                                                                                                                                                                                                                                                                                                                                                      5.0%; Score 16; DB 2; Length 289; 100.0%; Pred. No. 21; ive 0; Mismatches 0; Indels
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US-08-746-397-1/c
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                                                                                     TELEFAX: 201-994-1744
INFORMATION FOR SEQ ID NO: 1:
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                                                                                                             NAME: MULLINS, J.G.
REGISTRATION NUMBER: 33,073
REFERENCE/DOCKET NUMBER: 32
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-94-1700
                                                                         SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                          SOFTWARE: WORD PERFECT 5.1
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/08/7
FILING DATE: 11/8/96
CLASSIFICATION: 424
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 415-845-4166
INFORMATION FOR SEQ ID NO: 12:
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ATTORNEY/AGENT INFORMATION:
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MOLECULE TYPE: CDNA
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MEDIUM TYPE: 3.5 INCH DISKETTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: NI ET AL.
TITLE OF INVENTION: Human Stem Cell Antigen 2
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: CARELLA, BYRNE, BAIN, GILFILLAN,
ADDRESSEE: CECCHI, STEWART & OLSTEIN
STREET: 6 BECKER FARM ROAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
LENGTH: 335 base pairs
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LIBRARY: BRSTNG
CLONE: 637479
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REFERENCE/DOCKET NUMBER: PF
                           STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MOLECULE TYPE:
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APPLICATION NUMBER: US
                                                           LENGTH:
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16; Conservative
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                LINEAR
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+ tve 0; Mismatches
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100.0%; Pred. No.
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21;
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                                                                Matches
                                                                                             Query Match
                                                                                                                                                                                                     INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 115,
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                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 21
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM Compatible
OPERATING SYSTEM: IBM P.C.
SOFTWARE: WORD Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/
                                                                                                                                                                                                                                                                                                                      FILING DATE: October 18, 1994
ATTORNEY/AGENT INFORMATION:
NAME: BIGGS, SUZANNE L.
                                                                                                                                                                                                                                                                                                                                                                     FILING DATE: June 5, 1995

CLASSIFICATION: 530

PRIOR APPLICATION NOMBER: 08/326,110

APPLICATION NUMBER: 08/326,110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
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                                                                                                                                         TYPE: nucleic acid
STRANDEDNESS: sing
TOPOLOGY: linear
                                                               Local Similarity
les 15; Conserv
                                                                                                                                                                                                                                     TELEFAX: (213)
TELEX: 67-3510
                                                                                                                                                                                                                                                                                                           NAME: BIGGS, SUZANNE REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Lyon & Lyon
STREET: 633 West Fifth Street
STREET: Suite 4700
CITY: Los Angeles
STATE: California
                                                                                                                                                                                      LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDIUM TYPE: 3.5" Diskette, 1.44 Mb MEDIUM TYPE: storage
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP:
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              63 GATGGCCGACTTGGC 77
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GATGGCCGACTTGGC 44
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5863894
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                                                                                                                                                                                     45 base pairs
                                                             Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  George P. Vlasuk, Patric H. Stanssens, Joris H.L. Mensens, Marc J. Lauwereys, Yves R. Laroche, Laurent S. Jespers, Yannick G.J. Gansemans, Matthew Moyle,
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                                                                                                                                                                                                                                                  955-0440
                                                        4.7%; Score 15; DB 2;
100.0%; Pred. No. 74;
htive 0; Mismatches
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100.0%; Pred. No.
tive 0; Mismatc
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                                                                                                                                                                                                                                                                                                         30,158
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                                                                                       Length 45;
                                                          Indels
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                                                        Gaps
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; Sequence 30, Application US/08480478

US-08-480-478-30

RESULT 11

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                                                                                                                                                                                               Sequence 115, Application US/08486397 Patent No. 5866542
                                                                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 30
SEQUENCE CHARACTERISTICS:
LENGTH: 45 base pairs
                                                                                                                                                                                  GENERAL INFORMATION:
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MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: BIGGS, SUZANNE L.
REGISTION NUMBER: 30,158
REFERENCE/DOCKET NUMBER: 20
TELECOMMUNICATION INFORMATION:
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CURRENT APPLICATION DATA:
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FILING DATE: 18 OCTOBER 1994
ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES:
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                                APPLICANT: George P. Vlasuk, Patric H. Stanssens, APPLICANT: Joris H.L. Mensens, Marc J. Lawereys, APPLICANT: Yves R. Laroche, Laurent S. Jespers, APPLICANT: Yannick G.J. Gansemans, Matthew Moyle, APPLICANT: Peter W. Bergum TITLE OF INVENTION: BEASTODE-EXTRACTED ANTICOAGULANT TITLE OF INVENTION: PROTEIN NUMBER OF SEQUENCES: 357
               NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
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STATE: California
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ADDRESSEE: Lyon & Lyon
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633 West Fifth Street
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LIEVEN MESSENS; MARC JOZEF
LAUMEREYS; YVES RENE LAROCHE;
LAUMENT STEPHANE JESPERS; and
YANNICK GEORGES JOZEF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GEORGE P. VLASUK; PATRICK ERIC
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                                                                                                                                                                                                                                                                                                                                                                                     Conservative
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US-08-486-399-115
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: George P. Vlasuk, Patric H. Stanssens,
APPLICANT: Joris H.L. Mensens, Marc J. Lauwereys,
APPLICANT: Yees R. Laroche, Laurent S. Jespers,
APPLICANT: Yannick G.J. Gansemans, Matthew Moyle,
APPLICANT: Peter W. Bergum
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MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
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FILING DATE: October 18, 1994
ATTORNEY/AGENT INFORMATION:
NAME: BIGGS, SUZANNE L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FILING DATE: June 5, CLASSIFICATION: 530 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE CHARACTERISTICS:
LENGTH: 45 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
                                                                                                                                          ZIP: 90071
COMPUTER READABLE FORM:
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
MEDIUM TYPE: TRM Compatible
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                                      SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
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STATE: California
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TELEFAX: (213) 955-0440
TELEX: 67-3510
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                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Los Angeles
                                                                                                                                                                                                                                                                                                                                  COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                    STATE:
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APPLICATION NUMBER:
                                                                                                           OPERATING SYSTEM:
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633 West Fifth Street
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           US/08/486,399
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INFORMATION FOR SEQ ID NO: 115:
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TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 11
SEQUENCE CHARACTERISTICS:
LENGTH: 45 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                         APPLICATION NUMBER: 08/326,110
FILING DATE: October 18, 1994
ATTORNEY/AGENT INFORMATION:
NAME: BIGGS, SUZANNE L.
REGISTRATION NUMBER: 30,158
REFERENCE/DOCKET NUMBER: 210/243
                                                          TELECOMMUNICATION INFORMATION: TELEPHONE: (213) 489-1600
                                                                                                                                                                                                              CLASSIFICATION: 530 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                 OPERATING SYSTEM: IBM P.C. DOS 5.0
SOFTWARE: Word Perfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/461,965
FILING DATE: June 5, 1995
CTARSTETCATION. E.S. 1995
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COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CORRESPONDENCE ADDRESS:
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TITLE OF INVENTION: PROTEIN
NUMBER OF SEQUENCES: 356
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
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FILING DATE: October 18, 1994
ATTORNEY/AGENT INFORMATION:
NAME: BIGGS, SUZANNE L.
REGISTRATION NUMBER: 30,158
REGISTRATION NUMBER: 30,158
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CLASSIFICATION: 530
PRIOR APPLICATION DATA:
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STATE: California
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STREET: 633 West F:
STREET: Suite 4700
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                          67-3510
                                          (213) 955-0440
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Joris H.L. Mensens, Marc J. Lauwereys,
Yves R. Laroche, Laurent S. Jespers,
Yannick G.J. Gansemans, Matthew Moyle,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3: Lyon & Lyon
633 West Fifth Street
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                                     Query Match
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                                                                                                                                  TELEX: 67-3510
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 201
TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
NAME: BIGGS, SUZANNE L.
REGISTRATION NUMBER: 30,
                                                                                                                                                                                                                                                                                                                                                            SOFTWARE: FastSEQ Vers
CURRENT APPLICATION DATA:
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MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
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APPLICATION NUMBER:
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STREET: Suite 4700
CITY: Los Angeles
STATE: California
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APPLICANT:
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                                                                             STRANDEDNESS:
TOPOLOGY: lir
                                                                                                          TYPE:
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                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/326,110A FILING DATE: 18 OCTOBER 1994 CLASSIFICATION: 530
                                                                                                                                                                                                                                                                               FILING DATE:
                                                                                                                      LENGTH:
                                                                                                                                                                             TELEFAX:
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STRANDEDNESS: single
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Local Similarity 100.0%; Pred. No. /*/
Conservative 0; Mismatches
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                                                                                       nucleic acid
EDNESS: single
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        Conservative
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633 West Fifth Street
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LIEVEN MESSENS; MARC JOZEF
LAUWEREYS; YVES RENE LAROCHE;
LAURENT STEPHANE JESPERS; and
YANNICK GEORGES JOZEF
                                                                              linear
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30,158
                   4.7%; Score 15; DB 2; 100.0%; Pred. No. 74;
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COAGULANT PROTEIN
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Maximum DB seq length: 2000000000
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Copyright (c) 1993 - 2003 Compugen Ltd.
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US-09-796-692-3607

US-10-040-862-3737

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                                                                  Sequence 5769, Ap

Sequence 5769, Ap

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Sequence 5667, Ap

Sequence 5607, Ap
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-09-960-332-10/33	209-783-390-0003	10	-00-964-761-748	78	-09-833-381-1856	-92	1-92	925	2 4 2	2 4	5	-73	900	-76	760		900	-80	738.	-103	OTO	2 1	100	96	-983	-867	-934	-934	934	,
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ALIGNMENTS

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RESULT 1
US-09-918-995-19156
Sequence 19156, Application US/09918995
Publication No. US20030073623A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ; publication NO. US20
; GENERAL INFORMATION:
Fequence 20836, Application US/09918995
publication No. US20030073623A1
GENERAL INFORMATION:
APPLICANT: HYSEG, Inc.
TITLE OF INVENTION: NOVEL NUCLEIC ACID SEQUENCES OBTAINED;
TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES;
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                                                                                                                                             US-09-918-995-20836
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TITLE OF INVENTION: FROM VARIOUS CDNA LIBRARIES
CURRENT FILLING DATE: 2001-07-30
CURRENT FILLING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: US/09/235,076
PRIOR APPLICATION NUMBER: US/09/235,076
PRIOR FILLING DATE: 1999-01-20
NUMBER OF SEQ ID NOS: 38054
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 19156
                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 463
TYPE: DNA
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: misc_feature
LOCATION: (1)...(463)
OTHER INFORMATION: n = A,T,C or G
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                                                                                                                                                                                                                                      58 CCGTGCTGTCTGAACTC 74
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17; Conserva
                                                                                                                                                                                                                                                                                                                                    Conservative
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FILE REFERENCE: 20411-756

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US-09-712-363-25
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PRIOR FILING DATE: 2000-01-28
PRIOR APPLICATION NUMBER: 60/179,531
PRIOR APPLICATION NUMBER: 60/117,531
PRIOR APPLICATION NUMBER: 60/117,844
PRIOR APPLICATION NUMBER: 60/118,206,
PRIOR FILING DATE: 1999-01-29
PRIOR PILING DATE: 1999-02-01
PRIOR APPLICATION NUMBER: 60/126,593
PRIOR FILING DATE: 1999-03-26
PRIOR APPLICATION NUMBER: 60/126,593
PRIOR FILING DATE: 1999-03-26
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Sequence 25, Application US/09712363

Patent No. US20020164588A1
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CURRENT FILING DATE: 2001-07-30
PRIOR APPLICATION NUMBER: US/09/235,076
PRIOR FILING DATE: 1999-01-20
NUMBER OF SEQ ID NOS: 38054
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 20836
LENGTH: 484
ORGANISM: Homo sapiens
                                                                                     Matches
                                                                                                                    Query Match
                                                                                                                                                                                                                                     SEQ ID NO 25
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                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: 60/165,124
PRIOR FILING DATE: 1999-11-12
PRIOR APPLICATION NUMBER: 60/165,086
PRIOR FILING DATE: 1999-11-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Elsenberg, David
APPLICANT: Rotstein, Sergio H.
APPLICANT: Marcotte, Edward M.
TITLE OF INVENTION: DETERMINING THE FUNCTIONS AND
TITLE OF INVENTION: INTERACTIONS OF PROTEINS BY C
FILE REFERENCE: 07419-032001
CURRENT APPLICATION NUMBER: US/09/712,363
CURRENT FILING DATE: 2000-11-13
CURRENT FILING DATE: 2000-11-13
                                                                                                                                                                       TYPE: DNA
ORGANISM: Mycobacterium tuberculosis
                                                                                                                                                                                                                                                              SOFTWARE:
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                                                                                                                                                                                                                     LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY: misc_feature
LOCATION: (1)...(484)
OTHER INFORMATION: n = A,T,C or G
                                                                                 Local Similarity es 17; Conserv
                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: 60/134,092
FILING DATE: 1999-05-14
                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 60/134,093
FILING DATE: 1999-05-14
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876 GGCCGACTTGGCGCGCA 892
                                   66 GGCCGACTTGGCGCGCA 82
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                                                                             Conservative
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                                                                  100.08; +1
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                                                                                         5.3%; Score 17;
100.0%; Pred. No.
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US-10-040-862-5769/c
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; NAME/KEY: unsure
; LOCATION: (43)
; OTHER INFORMATION: n=A,T,C or G
US-09-796-692-5769
                                                                                                                                                                                                                                                Sequence 5769, Application US/10040862
Publication No. US20030078396A1
GENERAL INFORMATION:
APPLICANT: Mannion, Jane
APPLICANT: Metter, Marc
APPLICANT: Corixa Corporation
TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Ther
TITLE OF INVENTION: Hematological Malignancies
FILE REFERENCE: 014058-013520US
CURRENT APPLICATION NUMBER: US/10/040,862
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APPLICANT: Gaiger, Alexander
APPLICANT: Algate, Paul A.

APPLICANT: Mannion, Jane
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THER
TITLE OF INVENTION: HEMATOLOGICAL MALIGNANCIES
FILE REFERENCE: 2077.001200
CURRENT APPLICATION NUMBER: US/09/796,692
CURRENT FILING DATE: 2001-03-01
PRIOR APPLICATION NUMBER: 50/186,126
PRIOR FILING DATE: 2000-03-01
PRIOR FILING DATE: 2000-03-01
                                                                                                                                                                                                APPLICANT: Gaiger, Alexander APPLICANT: Algate, Paul A.
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SOFTWARE: PastSEQ for Windows Version 3.0
SEQ ID NO 5769
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: 60/223,416
PRIOR FILING DATE: 2000-08-04
PRIOR APPLICATION NUMBER: 60/223,378
PRIOR FILING DATE: 2000-08-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: 60/206, 201
PRIOR FILING DATE: 2000-05-22
PRIOR APPLICATION NUMBER: 60/218,950
PRIOR FILING DATE: 2000-07-14
PRIOR APPLICATION NUMBER: 60/212,903
DBTOR FILING DATE: 2000-07-14
DBTOR FILING DATE: 2000-07-14
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PRIOR FILING DATE: 2000-04-28
PRIOR APPLICATION NUMBER: 60/200,779
PRIOR FILING DATE: 2000-04-28
PRIOR APPLICATION NUMBER: 60/200,999
PRIOR FILING DATE: 2000-05-01
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: DNA
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PRIOR FILING DATE: 2000-03-17
PRIOR APPLICATION NUMBER: 60/200,545
PRIOR FILING DATE: 2000-04-27
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PRIOR FILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: US 60/200,303
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PRIOR APPLICATION NUMBER: US 60/186,126
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PRIOR APPLICATION NUMBER: US 6
PRIOR FILING DATE: 2000-08-04
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PRIOR FILING DATE: 2000-05-04
PRIOR APPLICATION NUMBER: US 60/206,201
PRIOR APPLICATION NUMBER: US 60/206,201
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 5723, Application US/09796692 publication No. US20020198362Al GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQ ID NOS: 10467
SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: US 60/223,378
PRIOR FILING DATE: 2000-08-07
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PRIOR FILING DATE: 2001-03-01
                                                                                                                                                                                               APPLICANT: Gaiger, Alexander APPLICANT: Adjate, Paul A.
APPLICANT: Adjate, Paul A.
APPLICANT: Adjate, Paul A.
APPLICANT: Mannion, Jane
APPLICANT: MAINTON: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THERAPY TITLE OF INVENTION: HEMATOLOGICAL MALIGNANCIES
TITLE OF INVENTION ON 1020
CURRENT PAPLICATION NUMBER: US/09/796,692
CURRENT FILING DATE: 2001-03-01
PRIOR APPLICATION NUMBER: 60/186,126
PRIOR APPLICATION NUMBER: 60/190,479
PRIOR APPLICATION NUMBER: 60/190,479
PRIOR APPLICATION NUMBER: 60/190,479
PRIOR FILING DATE: 2000-03-17
PRIOR FILING DATE: 2000-03-17
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                                                                                              PRIOR APPLICATION NUMBER: 60/200,545
PRIOR FILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: 60/200,303
PRIOR FILING DATE: 2000-04-28
PRIOR FILING DATE: 2000-04-28
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APPLICATION NUMBER: 60/200,779
FILING DATE: 2000-04-28
APPLICATION NUMBER: 60/200,999
FILING DATE: 2000-05-01
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16; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5.0%; Score 16; DB 9; Length 151; 100.0%; Pred. No. 32;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0,
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TYPE: DNA
ORGANISM: Homo sapiens
US-09-796-692-5723
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR FILING DATE: 2000-05-04
PRIOR APPLICATION NUMBER: 60/206,201
PRIOR FILING DATE: 2000-05-22
PRIOR APPLICATION NUMBER: 60/218,950
PRIOR APPLICATION NUMBER: 60/218,950
PRIOR FILING DATE: 2000-07-14
PRIOR FILING DATE: 2000-07-14
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                                                                                                                                                                                                                                          PRIOR FILLING DATE: 2000-04-28
PRIOR APPLICATION NUMBER: US 60/200,999
PRIOR APPLICATION NUMBER: US 60/200,999
PRIOR APPLICATION NUMBER: US 60/202,084
PRIOR APPLICATION NUMBER: US 60/202,084
PRIOR APPLICATION NUMBER: US 60/206,201
PRIOR FILING DATE: 2000-05-04
PRIOR APPLICATION NUMBER: US 60/206,201
PRIOR APPLICATION NUMBER: US 60/218,950
PRIOR PRILING DATE: 2000-05-12
PRIOR APPLICATION NUMBER: US 60/218,950
PRIOR FILING DATE: 2000-07-14
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PRIOR FILING DATE: 2000-08-04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 5723, Application US/10040862 Publication No. US20030078396A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: 60/222,903
PRIOR FILING DATE: 2000-08-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: FastSEQ for Windows Version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Ther TITLE OF INVENTION: Hematological Malignancles FILE OF INVENTION: Hematological Malignancles FILE REFERENCE: 014058-013520US CURRENT APPLICATION NUMBER: US/10/040,862 CURRENT FILING DATE: 2001-11-06 CURRENT FILING DATE: 2001-11-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Gaiger, Alexander APPLICANT: Algate, Paul A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: US 60/186,126
PRIOR EILING DATE: 2000-03-01
PRIOR APPLICATION NUMBER: US 60/190,479
PRIOR FILING DATE: 2000-03-17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 154
NUMBER OF SEQ ID NOS: 10467
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 5723
                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR FILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: US 60/200,303
PRIOR FILING DATE: 2000-04-28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION NUMBER: US 60/200,545
                                                                  PRIOR FILING DATE: 2000-08-07
PRIOR APPLICATION NUMBER: US 09/796,692
PRIOR FILING DATE: 2001-03-01
                                                                                                                                                                             PRIOR APPLICATION NUMBER: US 60/223,416
                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: US (PRIOR FILING DATE: 2000-08-03
                                                                                                                                                          PRIOR FILING DATE:
                                                                                                                                         PRIOR APPLICATION NUMBER:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22 GGATCCTCAGGCACCC 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16; Conservative
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Retter, Marc
Corixa Corporation
                                                                                                                                                                 2000-08-04
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[00.0%; Pred. No.
                                                                                                                                                US 60/223,378
                                                                                                                                                                                                                                        US 60/222,903
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32;
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LENGTH: 154

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APPLICANY. MANDION, Jane
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THERAPY
FILE REFERENCE: 2077.001200
CURRENT APPLICATION UNMBER: US/09/796,692
CURRENT FILING DATE: 2007.03.01
PRIOR APPLICATION NUMBER: 60/186,126
PRIOR APPLICATION NUMBER: 60/190,479
PRIOR FILING DATE: 2000.03.17
PRIOR APPLICATION NUMBER: 60/200,545
PRIOR APPLICATION NUMBER: 60/200,545
PRIOR APPLICATION NUMBER: 60/200,303
PRIOR APPLICATION NUMBER: 60/200,303
PRIOR APPLICATION NUMBER: 60/200,779
PRIOR APPLICATION NUMBER: 60/200,799
PRIOR APPLICATION NUMBER: 60/200,999
PRIOR RILING DATE: 2000-04-28
PRIOR APPLICATION NUMBER: 60/200,999
PRIOR FILING DATE: 2000-05-01
PRIOR FILING DATE: 2000-05-04
PRIOR APPLICATION NUMBER: 60/202,084
PRIOR FILING DATE: 2000-05-04
PRIOR FILING DATE: 2000-05-04
PRIOR APPLICATION NUMBER: 60/202,084
PRIOR FILING DATE: 2000-05-02
PRIOR APPLICATION NUMBER: 60/202,084
PRIOR FILING DATE: 2000-05-02
PRIOR APPLICATION NUMBER: 60/202,084
PRIOR APPLICATION NUMBER: 60/202,093
PRIOR APPLICATION NUMBER: 60/202,378
Sequence 5607, Application US/09796692
Publication No. US20020198362A1
GENERAL INFORMATION:
                                                                                         US-09-796-692-5607
                                                                                                                        RESULT 9
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US-09-796-692-3737
Sequence 3737, Application No. US2002
Publication No. US2002
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                     Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS: 9597
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 3737
LENGTH: 158
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Gaiger, Alexander
APPLICANT: Algate, Paul A.
APPLICANT: Mannion, Jane
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                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                        133 GGATCCTCAGGCACCC 148
                                                                                                                                                                                                                                         166 GGATCCTCAGGCACCC 181
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                                                                                                                                                                                                                                                                                                        16; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2000-08-07
os: 9597
                                                                                                                                                                                                                                                                           5.0%; Score 16; DB 9; Length 158; 100.0%; Pred. No. 32; Indels
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100.0%; Pred. No.
ative 0; Mismatc
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APPLICANT: Algate, paul A.

APPLICANT: Mannion, Jane
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THER
TITLE OF INVENTION: HEMATOLOGICAL MALIGNANCIES
CURRENT ELICATION NUMBER: US/09/796,692
CURRENT APPLICATION NUMBER: 60/196,692
PRIOR APPLICATION NUMBER: 60/186,126
PRIOR APPLICATION NUMBER: 60/190,479
PRIOR APPLICATION NUMBER: 60/190,479
PRIOR APPLICATION NUMBER: 60/190,479
PRIOR APPLICATION NUMBER: 60/200,545
PRIOR APPLICATION NUMBER: 60/200,545
PRIOR APPLICATION NUMBER: 60/200,709
PRIOR APPLICATION NUMBER: 60/200,709
PRIOR APPLICATION NUMBER: 60/200,709
PRIOR APPLICATION NUMBER: 60/200,709
PRIOR FILING DATE: 2000-04-28
PRIOR APPLICATION NUMBER: 60/200,779
PRIOR APPLICATION NUMBER: 60/200,779
PRIOR APPLICATION NUMBER: 60/200,779
PRIOR FILING DATE: 2000-04-28
PRIOR APPLICATION NUMBER: 60/200,770
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; ORGANISM: Homo sapiens
US-09-796-692-5607
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CURRENT FILING DATE: 2001-03-01
PRIOR APPLICATION NUMBER: 60/186,126
PRIOR ETLING DATE: 2000-03-01
PRIOR PELLING DATE: 2000-03-01
PRIOR PELLING DATE: 2000-03-01
PRIOR PELLING DATE: 2000-04-27
PRIOR PELLING DATE: 2000-04-27
PRIOR PELLING DATE: 2000-04-27
PRIOR PELLING DATE: 2000-04-28
PRIOR PELLING DATE: 2000-04-28
PRIOR PELLING DATE: 2000-04-29
PRIOR PELLING DATE: 2000-04-29
PRIOR APPLICATION NUMBER: 60/200,779
PRIOR APPLICATION NUMBER: 60/200,999
PRIOR APPLICATION NUMBER: 60/200,999
PRIOR PELLING DATE: 2000-05-01
PRIOR PELLING DATE: 2000-05-01
PRIOR PELLING DATE: 2000-05-01
PRIOR PELLING DATE: 2000-05-02
PRIOR PELLING DATE: 2000-05-03
PRIOR PELLING DATE: 2000-05
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Publication No. US20020198362A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Gaiger, Alexander APPLICANT: Algate, Paul A. APPLICANT: Mannion, Jane
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Best Local
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PRIOR FILING DATE: 2000-08-04
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APPLICANT: Mannion, Jane
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THER
FILE REFERENCE: 2077.001200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Gaiger, Alexander
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity
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100.0%; Pred. No. 32;
ative 0; Mismatches
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-796-692-5667
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US-10-040-862-3737
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LENGTH: 158
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PRIOR APPLICATION NUMBER: 60/206,201
PRIOR FILING DATE: 2000-05-22
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PRIOR FILING DATE: 2000-08-07
NUMBER OF SEQ ID NOS: 9597
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APPLICANT: Algate, Paul A.
APPLICANT: Mannion, Jane
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CURRENT FILING DATE: 2001-11-06
PRIOR APPLICATION NUMBER: US 60/186,126
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PRIOR APPLICATION NUMBER: US 60/200,303
PRIOR FILING DATE: 2000-04-28
PRIOR APPLICATION NUMBER: US 60/200,779
PRIOR FILING DATE: 2000-04-28
PRIOR FILING DATE: 2000-04-28
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PRIOR APPLICATION NUMBER: US 60/190,479
PRIOR FILING DATE: 2000-03-17
PRIOR FILING DATE: 1000-03-17
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                                                                                                                                             PRIOR APPLICATION NUMBER: US 60/223,416
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PRIOR APPLICATION NUMBER: US 60/222,903
                                     PRIOR APPLICATION NUMBER: US 09/796,692 PRIOR FILING DATE: 2001-03-01
                                                                               PRIOR FILING DATE:
                                                                                 PRIOR APPLICATION NUMBER: US 60/223,378 PRIOR FILING DATE: 2000-08-07
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NUMBER OF SEQ ID NOS: 10467
SOFTWARE: FastSEQ for Windows Version 3.0
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Corixa Corporation
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100.0%; Pred. No.
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; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-040-862-3737
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US-10-040-862-5607
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TITLE OF INVENTION: Hematological Malignancies
FILE REFERENCE: 014058-013520US
                                                                                                                                                                                                                               SEQ ID NO 5607
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: US 60/200,779
PRIOR FILING DATE: 2000-04-28
PRIOR APPLICATION NUMBER: US 60/200,999
PRIOR FILING DATE: 2000-05-01
PRIOR APPLICATION NUMBER: US 60/202,084
PRIOR APPLICATION NUMBER: US 60/202,084
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PRIOR FILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: US 60/200,303
PRIOR FILING DATE: 2000-04-28
PRIOR FILING DATE: 2000-04-28
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CURRENT FILING DATE: 2001-11-06
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PRIOR APPLICATION NUMBER: US 60/206,201
PRIOR FILING DATE: 2000-05-22
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SOFTWARE: FastSEQ for Windows Version 3.0
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PRIOR APPLICATION NUMBER: US 09/796,692
PRIOR FILING DATE: 2001-03-01
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PRIOR APPLICATION NUMBER: US 60/222,903
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ORGANISM: Homo sapiens
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133 GGATCCTCAGGCACCC 148
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Corixa Corporation
                                                                        Conservative
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100.0%; Pred. No.
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100.0%; Pred. No.
tive 0; Mismatch
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RESULT 14
US-09-796-692-6280
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; ORGANISM: Homo sapiens
US-10-040-862-5667
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APPLICANT: Algate, Paul A.
APPLICANT: Algate, Paul A.
APPLICANT: Mannion, Jane
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE DETECTION, DIAGNOSIS AND THERAPY
TITLE OF INVENTION: HEMATOLOGICAL MALIGNANCIES
FILE REFERENCE: 2077.001200
CURRENT APPLICATION NUMBER: US/09/796,692
CURRENT FILING DATE: 2001-03-01
PRIOR APPLICATION NUMBER: 60/186,126
PRIOR FILING DATE: 2000-03-01
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CURRENT FILING DATE: 2001-11-06
PRIOR APPLICATION NUMBER: US 60/186,126
PRIOR FILING DATE: 2000-03-01
PRIOR APPLICATION NUMBER: US 60/190,479
PRIOR FILING DATE: 2000-03-17
PRIOR APPLICATION NUMBER: US 60/200,545
PRIOR FILING DATE: 2000-04-27
PRIOR PRIOR PRIOR DATE: 2000-04-28
PRIOR FILING DATE: 2000-04-28
PRIOR FILING DATE: 2000-04-28
PRIOR FILING DATE: 2000-04-28
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PRIOR FILING DATE: 2000-05-01
PRIOR APPLICATION NUMBER: US 60/202,084
PRIOR FILING DATE: 2000-05-04
PRIOR PRIOR FILING DATE: 2000-05-22
PRIOR FILING DATE: 2000-05-22
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PRIOR FILING DATE: 2000-04-28
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APPLICATION NUMBER: US 60/223,378
FILING DATE: 2000-08-07
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Corixa Corporation
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100.0%; Pred. No.
tive 0; Mismatc
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PRIOR APPLICATION NUMBER: US 60/200,303
PRIOR FILING DATE: 2000-04-28
PRIOR APPLICATION NUMBER: US 60/200,779
PRIOR APPLICATION NUMBER: US 60/200,779
PRIOR APPLICATION NUMBER: US 60/200,999
PRIOR FILING DATE: 2000-05-01
PRIOR APPLICATION NUMBER: US 60/202,084
PRIOR FILING DATE: 2000-05-04
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; ORGANISM: Homo sapiens
; FEATUREM:
; KATUREM: Unsure
; NAME/KEY: unsure
; COCATION: (1)
; OTHER INFORMATION: n-A,T,C or G
US-09-796-692-6280
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APPLICANT: Gaiger, Alexander
APPLICANT: Algate, Paul A.
                                                                                                                                                                                                           CURRENT APPLICATION NUMBER: US/10/040,862 CURRENT FILING DATE: 2001-11-06 PRIOR APPLICATION NUMBER: US 60/186,126 PRIOR FILING DATE: 2000-03-01 PRIOR APPLICATION NUMBER: US 60/190,479 PRIOR FILING DATE: 2000-03-17
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APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 6280, Application US/10040862
Publication No. US20030078396A1
                                                                                                                                                                                                                                                                                                                       APPLICANT: Retter Marc
APPLICANT: Corixa Corporation
TITLE OF INVENTION: Compositions and Methods for the Detection, Diagnosis and Ther
TITLE OF INVENTION: Hematological Malignancies
FILE REFERENCE: 014058-013520US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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SEQ ID NO 6280
LENGTH: 159
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PRIOR FILING DATE: 2000-08-04
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PRIOR FILING DATE: 2000-03-17
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PRIOR APPLICATION NUMBER: US 60/223,378

PRIOR APPLICATION NUMBER: US 09/796,692

PRIOR FILING DATE: 2000-08-07

PRIOR FILING DATE: 2001-03-01

PRIOR APPLICATION NUMBER: US 09/796,692

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PRIOR APPLICATION NUMBER: US 09/796,692

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ALIGNMENTS

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RESULT 1
AAU97552
Mercuric ion; contaminated soil; ground water; hydroponic solution; irrigation water; waste stream; contaminated aqueous medium; biological fluid; gastrointestinal tract; chelon protein; enteric bacteria; toxic metal ion; mercury; cadmium; divalent catio
                       WPI; 2002-435437/46.
                                                                                                                                 18-APR-2002.
                                                                                                                                                                           Synthetic.
                                                                                                                                                                                                                                                                  Synthetic MerR chelon variant.
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                                            Summers AO,
                                                                                      12-OCT-2000; 2000US-240465P.
                                                                                                           12-OCT-2001; 2001WO-US31819
                                                                                                                                                       WO200230962-A2.
                                                                                                                                                                                                 heavy metal binding protein; MerR.
                                                                 (UYGE-)
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RESULT 2
AAU97560
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Crahe nucleic acid encoding the chelon protein is useful for binding credit mercuric ions, to take up, sequester and concentrate the heavy metal ions from contaminated soil, ground water, hydroponic solutions or immobilised onto a solid support, is useful for concentrating heavy metal consistent mercuric particular to suseful for concentrating heavy metal consistent medium including biological fluids. The nucleic acid, when recombinantly expressed in enteric bacteria (which are nontoxigenic and compathogenic), is suitable for use in the in vivo sequestration and claimination of mercuric ion from gastrointestinal tracts of animals or molecules of the invention are also useful in water treatment resins. The nucleic acid of the invention is highly specific and binds divalent cration such as mercury or cadmium with high affinity. The present amino contented chalons of the invention is highly specific and binds divalent cald sequence represents the synthetic Merk chelon variant protein of the invention. This sequence is one of the heavy metal binding proteins contented chalons of the invention are dead in the protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Matches
12-OCT-2000; 2000US-240465P
                                              12-OCT-2001; 2001WO-US31819.
                                                                                           18-APR-2002
                                                                                                                                       WO200230962-A2
                                                                                                                                                                                                                                                                     Mercuric ion; contaminated soil; ground water; hydroponic solution; irrigation water; waste stream; contaminated aqueous medium; biological fluid; gastrointestinal tract; chelon protein;
                                                                                                                                                                                                                                                                                                                                                                Synthetic cadmium/mercury ion binding chelon protein #8
                                                                                                                                                                                                                              heavy metal binding protein.
                                                                                                                                                                                                                                                   enteric bacteria; toxic metal ion; mercury;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAU97560;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAU97560 standard; Protein; 117 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         which binds mercuric ions. The invention is useful for recombinantly producing a protein in a host-cell, by infecting or transforming a h
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention relates to a new non-naturally occurring recombinant DNA molecule comprising a sequence encoding a chelon protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Claim 2; Page 20; 42pp; English.
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mes 117; Conser
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ilarity 100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        which binds mercuric ions. The invention is useful for recombinantly conducing a protein in a host-cell, by infecting or transforming a host cell capable of expressing a chelon coding sequence with a vector comprising a promoter active in the host cell operably linked to a coding region for the protein to produce a recombinant host cell and culturing the recombinant host cell under conditions, where DNA is expressed. The nucleic acid encoding the chelon protein is useful for binding cd divalent mercuric ions, to take up, sequester and concentrate the heavy metal ions from contaminated soil, ground water, hydroponic solutions or irrigation water of waste streams. The DNA of the invention, when close from contaminated environment waste streams or contaminated aqueous medium including biological fluids. The nucleic acid, when recombinantly expressed in enteric bacteria (which are nontoxigenic and conpathogenic), is suitable for use in the in vivo sequestration and elimination of mercuric ion from gastrointestinal tracts of animals or humans exposed to toxic metal ions such as mercury and/or cadmium. The calid sequence represents one of a collection (AA097553-AA097560) of cold sequence is one of the heavy metal binding proteins of the invention. This sequence is one of the heavy metal binding proteins termed chelons of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                 irrigation water; waste stream; contaminated aqueous medium;
biological fluid; gastrointestinal tract; chelon protein;
enteric bacteria; toxic metal ion; mercury; cadmium; divalent cation;
                                                                                                                                                                Synthetic cadmium/mercury ion binding chelon protein #1.
                                                                                                                                                                                                                                                                                    AAU97553 standard; Protein; 117 AA
                                                  heavy metal binding protein.
                                                                                                                               Mercuric ion;
                                                                                                                                                                                                         13-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 4; Page 22; 42pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Novel non-naturally occurring recombinant DNA molecule encoding a chelon protein useful for binding divalent cation mercury from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The present invention relates to a new non-naturally occurring recombinant DNA molecule comprising a sequence encoding a chel-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                contaminated soil, water, aqueous medium including biological fluids
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                                                                                                                                                                                                                                                                                                                                                                                                                    114 QFEK 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                   64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                       (first entry)
                                                                                                                           contaminated soil; ground water; hydroponic solution;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            54.7%; Score 64; 100.0%; Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1.8e-59;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 117;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     a chelon protein
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Comprising a protein in a host-cell, by infecting or transforming a host cell capable of expressing a chelon coding sequence with a vector comprising a promoter active in the host cell operably linked to a coding comprising a promoter active in the host cell operably linked to a coding cregion for the protein to produce a recombinant host cell and culturing the recombinant host cell under conditions, where DNA is expressed. The nucleic acid encoding the chelon protein is useful for binding created ions from contaminated soil, ground water, hydroponic solutions or irrigation water of waste streams. The DNA of the invention, when contaminated environment waste streams or contaminated contaminated environment waste strea
В
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12-OCT-2000; 2000US-240465P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention relates to a new non-naturally occurring
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 4; Page 22; 42pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (UYGE-) UNIV GEORGIA RES FOUND INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         recombinant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence
                  irrigation water; waste stream; contaminated aqueous medium; biological fluid; gastrointestinal tract; chelon protein; enteric bacteria; toxic metal ion; mercury; cadmium; divalent cation;
                                                                                                                                               Synthetic cadmium/mercury ion binding chelon protein #3.
                                                                                                                                                                                                   13-AUG-2002 (first entry)
                                                                                                                                                                                                                                            AAU97555:
                                                                                                                                                                                                                                                                                                AAU97555 standard; Protein; 117 AA
                                                                                        Mercuric ion; contaminated soil; ground water; hydroponic solution;
heavy metal binding protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local
                                                                                                                                                                                                                                                                                                                                                                                                                   l Similarity
57; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA molecule comprising a sequence encoding a chelon protein mercuric ions. The invention is useful for recombinantly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      117 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             48.7%; Score 57; DB 23; 100.0%; Pred. No. 4.2e-52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4.2e-52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 117;
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YXX PROS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CC which binds mercuric lons. The invention is useful for broducing a protein in a host-cell, by infecting or transforming a host cell producing sequence with a vector comprising a promoter active in the host cell operably linked to a coding comprising a promoter active in the host cell operably linked to a coding comprising a promoter active in the host cell operably linked to a coding cregion for the protein to produce a recombinant host cell and culturing the recombinant host cell under conditions, where DNA is expressed.

CC The nucleic acid encoding the chelon protein is useful for binding cometal ions from contaminated soil, ground water, hydroponic solutions or metal ions from contaminated soil, ground water, hydroponic solutions or contaminated environment waste streams or contaminated compact from contaminated environment waste streams or contaminated compact of the invention and content property is suitable for use in the in vivo sequestration and content property is suitable for use in the in vivo sequestration and content property is suitable for use in the in vivo sequestration and content property is suitable for use in the in vivo sequestration and content property is suitable for use in the in vivo sequestration and content property is suitable for use in the in vivo sequestration and content property is suitable for useful in water treatment resins.

CC molecules of the invention are also useful in water treatment resins.

CC molecules of the invention are also useful in water treatment resins.

CC molecules of the invention are also useful in water treatment resins.

CC molecules of the invention is highly specific and binds divalent among the property in the property of the invention is highly specific and binds divalent and content content content in the invention.

CC acid sequence represents one of a collection (AAU9753-AAU97560) of a fit is invention.
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XXX DXXX
                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel non-naturally occurring recombinant DNA molecule encoding a chelon protein useful for binding divalent cation mercury from contaminated soil, water, aqueous medium including biological fluids -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12-OCT-2000; 2000US-240465P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Summers AO,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (UYGE-) UNIV GEORGIA RES FOUND INC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Claim 4; Page 22; 42pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    recombinant DNA molecule comprising a sequence encoding a chelon protein which binds mercuric ions. The invention is useful for recombinantly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                             Synthetic cadmium/mercury ion binding chelon protein #4.
                                                                                                                                                                                                  AAU97556 standard; Protein; 117 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         of the invention.
                     Mercuric ion; contaminated soil; ground water; hydroponic solution;
                                                                                                               13-AUG-2002
                                                                                                                                                       AAU97556;
                                                                                                                                                                                                                                                                                                               Local
                                                                                                                                                                                                                                                                                                                                                                                                            57;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 117 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Caguiat JJ;
                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                         48.7%; Score 57; DB 23;
100.0%; Pred. No. 4.2e-5:
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                      4.2e-52;
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0;

irrigation water; waste stream; contaminated aqueous medium;

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The present invention relates to a new non-naturally occurring CC recombinant DNA molecule comprising a sequence encoding a chelon protein CC which binds mercuric ions. The invention is useful for recombinantly CC which binds mercuric ions. The invention is useful for recombinantly CC which producing a protein in a host-cell, by infecting or transforming a host CC cell capable of expressing a chelon coding sequence with a vector CC cell capable of expressing a chelon coding sequence with a vector CC region for the protein to produce a recombinant host cell and culturing CC the recombinant host cell under conditions, where DNA is expressed.

CC The nucleic acid encoding the chelon protein is useful for binding CC metal ions from contaminated soil, ground water, hydroponic solutions or CC irrigation water of waste streams. The DNA of the invention, when CC irrigation water of waste streams. The DNA of the invention or CC irrigation water of waste streams. The DNA of the invention are associated any invention and concentrating heavy metal capable for useful for concentrating heavy metal CC auceous medium including biological fluids. The nucleic acid, when CC elimination of mercuric ion from gastrointestinal tracts of animals or CC elimination of mercuric ion from gastrointestinal tracts of animals or CC molecules of the invention are also useful in water treatment resins. CC cation such as mercury or cadmium with high affinity. The present amino CC acid sequence represents one of a collection (AAN97553-AAN97560) of CC This sequence is one of the heavy metal binding ordeins termed chalons.
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Synthetic cadmium/mercury ion binding chelon protein #5
                                                                                                                       AAU97557 standard; Protein; 117 AA
                                                13-AUG-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                              of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 4; Page 22; 42pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel non-naturally occurring recombinant DNA molecule encoding a chelon protein useful for binding divalent cation mercury from contaminated soil, water, aqueous medium including biological fluids -
                                                                                                                                                                                                               WPI; 2002-435437/46.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           heavy metal binding protein.
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enteric bacteria; toxic metal ion; mercury; cadmium; divalent cation;
                                                                                                                                                                                                                                                                                                                                Local
                                                                                                                                                                                                                                                                                                                                                                                                                                  sequence is one of the heavy metal binding proteins termed chelons
                                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                                                                                                                                                                                                                                                                                                        117 AA;
                                                                                                                                                                                                                                                                                                         Conservative
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                                                                                                                                                                                                                                                                                                    48.7%; Score 57;
100.0%; Pred. No
tive 0; Mismato
                                                                                                                                                                                                                                                                                                                         Pred. No.
                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                                     DB 23; 1
                                                                                                                                                                                                                                                                                                                                    Length 117;
                                                                                                                                                                                                                                                                                                Indels
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29 ETYLSELYCACHARKGNYSCPLIASLQGSSGTHCEEASSLAEHKLKDYREKMADLAR 85

Matches Query Match Best Local (

57;

Conservative

48., 100.08; Fi 0;

48.7%; Score 57; DB 23; 100.0%; Pred. No. 4.2e-5 Mismatches

4.2e-52;

Length 117; Indels

0;

Gaps

0,

Similarity

AAU97558

AAU97558 standard; Protein; 117 AA.

AAU97558;

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divalent mercuric ions, to take up, sequester and concentrate the heavy content in the content i
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                                                                     of the invention
                                                                            This sequence is one of the heavy metal binding proteins termed chelons
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present invention relates to a new non-naturally occurring recombinant DNA molecule comprising a sequence encoding a chelon protein which blinds mercuric ions. The invention is useful for recombinantly producing a protein in a host-cell, by infecting or transforming a host cell capable of expressing a chelon coding sequence with a vector comprising a promoter active in the host cell operably linked to a coding the recombinant host cell under conditions, where DNA is expressed. The nucleic acid encoding the chelon protein is useful for binding the chelon protein is useful for binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 4; Page 22; 42pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel non-naturally occurring recombinant DNA molecule encoding a chelon protein useful for binding divalent cation mercury from contaminated soil, water, aqueous medium including biological fluids -
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117 AA;
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13-AUG-2002 (first entry)

Synthetic cadmium/mercury ion binding chelon protein

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                                                                                                                                                                                                                                                                                                                       The nucleic acid encoding the chelon protein is useful for binding contained to take up, sequester and concentrate the heavy contained soil, ground water, hydroponic solutions or irrigation water of waste streams. The DNA of the invention, when contaminated environment waste streams or concentrating heavy metal ions from contaminated environment waste streams or contaminated concentrating heavy metal consumer including biological fluids. The nucleic acid, when compathogenic, is suitable for use in the in vivo sequestration and contamination of mercuric ion from gastrointestinal tracts of animals or contaminated contains exposed to toxic metal ions such as mercury and/or cadmium. The nucleic acid of the invention are also useful in water treatment resins. The nucleic acid of the invention is highly specific and binds divalent contains contains contains contains a mercury one of a collection (AAU9753-AAU97560) of contains conta
                                                                                                           Matches
                                                                                                                                                          Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    producing a protein in a host-cell, by infecting or transforming a host cell capable of expressing a chelon coding sequence with a vector comprising a promoter active in the host cell operably linked to a coding region for the protein to produce a recombinant host cell and culturing the recombinant host cell under conditions, where DNA is expressed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            irrigation water; waste stream; contaminated aqueous medium;
biological fluid; gastrointestinal tract; chelon protein;
enteric bacteria; toxic metal ion; mercury; cadmium; divalent cation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel non-naturally occurring recombinant DNA molecule encoding a chelon protein useful for binding divalent cation mercury from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 4; Page 22; 42pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   contaminated soil, water, aqueous medium including biological fluids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 2002-435437/46
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mercuric ion; contaminated soil; ground water; hydroponic solution;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               heavy metal binding protein.
                                                                                                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      which binds
29
                             29 ETVLSELVCACHARKGNVSCPLIASLQGSSGTHCEEASSLAEHKLKDVREKMADLAR 85
                                                                                                                                                                                                                                                                               the invention.
                                                                                                                                                                                                                                                                                                         sequence is one of the heavy metal binding proteins termed chelons
ETVLSELVCACHARKGNVSCPLIASLQGSSGTHCEEASSLAEHKLKDVREKMADLAR
                                                                                                           l Similarity
57; Conser
                                                                                                                                                                                                                    117 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mercuric ions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             invention relates to a new non-naturally occurring
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA molecule comprising a sequence encoding a chelon protein mercuric ions. The invention is useful for recombinantly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Caguiat
                                                                                                              Conservative
                                                                                                                                      48.7%;
100.0%;
                                                                                                                                      Score 57; pred. No.
                                                                                                              0;
                                                                                                              Mismatches
                                                                                                                                         4.2e-52;
                                                                                                                                                                   DB 23;
                                                                                                                                                                Length 117
                                                                                                              Indels
                                                                                                              0;
     85
                                                                                                              Gaps
                                                                                                              0
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AAU97559 ID AAU9

AAU97559 standard; Protein; 117

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밁 ρy

48

48 CPLIASLQGSSGTHCEEASSLAEHKLKDVREKMADLARMETVLSELVCACHARKGNV 104

104

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cc which binds mercuric runs. The invention is useful for recombinantly protein in a host-cell, by infecting or transforming a host cell capable of expressing a chelon coding sequence with a vector comprising a promoter active in the host cell operably linked to a coding cregion for the protein to produce a recombinant host cell and culturing combinant host cell under conditions, where DNA is expressed. The nucleic acid encoding the chelon protein is useful for binding combinant mercuric ions, to take up, sequester and concentrate the heavy compared to the invention water of waste streams. The DNA of the invention, when crimpation water of waste streams. The DNA of the invention water contaminated soil, ground water, hydroponic solutions or contaminated environment waste streams or contaminated compathogenic), is suitable for useful fulds. The nucleic acid, when crecombinantly expressed in enteric bacteria (which are nontoxigenic and compathogenic), is suitable for use in the in vivo sequestration and compathogenic), is suitable for use in the in vivo sequestration and compathogenic), is suitable for use in the in value treatment resins. The nucleic acid of the invention are also useful in water treatment resins. The contains such as mercury and/or cadmium. The contains such as mercury and/or cadmium to cate in the invention and contains and contai
     Matches
                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             irrigation water; waste stream; contaminated aqueous medium;
biological fluid; gastrointestinal tract; chelon protein;
enteric bacteria; toxic metal ion; mercury; cadmium; divalent cation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel non-naturally occurring recombinant DNA molecule encoding a chelon protein useful for binding divalent cation mercury from contaminated soil, water, aqueous medium including biological fluids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic cadmium/mercury ion binding chelon protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         heavy metal binding protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mercuric ion; contaminated soil;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAU97559;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2002-435437/46
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                                                                                                 Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  which binds
                           Local
l Similarity
57; Conserv
                                                                                                                                                 invention.
                                                                                                 117 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DNA molecule comprising a sequence encoding a chelon promercuric ions. The invention is useful for recombinantly
       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (first entry)
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48.,
100.08; F1
  score 57; DB; Pred. No. 4.2.0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ground water; hydroponic solution;
       DB 23; 1
4.2e-52;
thes 0;
                                                    Length 117;
          Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             a chelon protein
       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 to a coding
          Gaps
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                                                                                                                                      CC which binds mercuric ions. The invention is useful for recombinantly cell capable of expressing a chelon coding sequence with a vector comprising a promoter active in the host cell operably linked to a coding region for the protein to produce a recombinant host cell and culturing the recombinant host cell under conditions, where DNA is expressed. CC The nucleic acid encoding the chelon protein is useful for binding cd divalent mercuric ions, to take up, sequester and concentrate the heavy metal ions from contaminated soil, ground water, hydroponic solutions or irrigation water of waste streams. The DNA of the invention, when combinantly expressed in enteric bacteria (which are nontoxigenic and compathogenic), is suitable for use in the in vivo sequestration and celimination of mercuric ion from gastrointestinal tracts of animals or humans exposed to toxic metal ions such as mercury and/or cadmium. The cation such as mercury or cadmium with high affinity. The present amino of a cation such as mercury or admium with high affinity. The present amino can an exposed to toxic metal ions such as finity. The present amino can are also useful affinity. The present amino can are also mercury wild-type metal and compathogenic and the invention are also useful in water treatment resins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 9
AAU97551
                                                              Matches
                                                                                                 Query Match
                                                                                                                                    Sequence
                                                                                                                                                             acid sequence represents the Shigella flexneri wild-type MerR protein of theinvention. This sequence was used in the methods of the invention for production of heavy metal binding proteins termed chelons.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention relates to a new non-naturally occurring recombinant DNA molecule comprising a sequence encoding a chelon protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 20; 42pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel non-naturally occurring recombinant DNA molecule encoding a chelon protein useful for binding divalent cation mercury from contaminated soil, water, aqueous medium including biological fluids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (UYGE-) UNIV GEORGIA RES FOUND INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         irrigation water;
biological fluid;
enteric bacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mercuric ion; contaminated soil; ground water; hydroponic
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAU97551 standard; Protein; 144 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      12-OCT-2001; 2001WO-US31819
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        heavy metal binding
                                                                             госат
               2 THCEEASSLAEHKLKDVREKMADLARMETVLSELVCACHARKGNVSCPLIASLQG 56
2002-435437/46
                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ΑO,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ABK52206
                                                                                                                                    144 AA;
                                                            Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      waste stream; contaminated aqueous medium; gastrointestinal tract; chelon protein; toxic metal ion; mercury; cadmium; divalent cation; ng protein; MerR.
                                                                             100.0%;
                                                                                             47.0%;
                                                          0
                                                                                             Score 55;
                                                                             Pred. No.
                                                        Mismatches
                                                        6.4e-50;
                                                                                             DB 23;
                                                                                         Length 144
                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          solution;
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                                                    Gaps
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KXEKKEFFFKKKOOOOOOOOOOOOOOOOOOOOOOO
                                                                                                                                           C divalent mercuric ions, to take up, sequester and concentrate the heavy metal ions from contaminated soil, ground water, hydroponic solutions or irrigation water of waste streams. The DNA of the invention, when c immobilised onto a solid support, is useful for concentrating heavy metal cons from contaminated environment waste streams or contaminated concentrating heavy metal consistency medalum including biological fluids. The nucleic acid, when crecombinantly expressed in enteric bacteria (which are nontoxigenic and compathogenic), is suitable for use in the in vivo sequestration and conpathogenic), is suitable for use in the in vivo sequestration and conpathogenic), is suitable for use in the invito sequestration and conpathogenic), is suitable for use in the invito sequestration and conpathogenic), is suitable for use in the invito acquisit of animals or compathogenic), is suitable for use in the inventory and/or cadmium. The model of the invention are also useful in water treatment resins.

CC molecules of the invention are also useful in water treatment resins.

CC The nucleic acid of the invention is highly specific and binds divalent contains such as mercury or cadmium with high affinity. The present amino acid sequence represents one of a collection (AAU97553-AAU97560) of avertheric cadmium/marcurv ion binding chalon professions of the invention is highly specific and binds divalent contains and the invention acid sequence represents one of a collection (AAU97553-AAU97560) of avertheric cadmium/marcurv ion binding chalon professions of the invention is highly specific and binds divalent contains and the invention acid sequence represents one of a collection (AAU97553-AAU97560) of avertheric cadmium/marcurv ion binding chalon professions.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               recombinant DNA molecule comprising a sequence encoding a chelon protein which binds mercuric ions. The invention is useful for recombinantly producing a protein in a host-cell, by infecting or transforming a host cell capable of expressing a chelon coding sequence with a vector comprising a promoter active in the host cell operably linked to a coding region for the protein to produce a recombinant host cell and culturing the recombinant host cell under conditions, where DNA is expressed. The nucleic acid encoding the chelon protein is useful for binding the chelon protein the conditions.
                                                                     of the
                                                                                                  This sequence is one
                                                                                                                                synthetic cadmium/mercury ion binding chelon proteins of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel non-naturally occurring recombinant DNA molecule encoding a chelon protein useful for binding divalent cation mercury from contaminated soil, water, aqueous medium including biological fluids -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The present invention relates to a new non-naturally occurring
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 4; Page 22; 42pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2002-435437/46
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biological fluid; gastrointestinal tract; chelon protein;
enteric bacteria; toxic metal ion; mercury; cadmium; divalent cation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic cadmium/mercury ion binding chelon protein #2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAU97554;
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                                                                 invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Caguiat JJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2001WO-US31819
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                                                                                               of the heavy metal binding proteins termed chelons
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Best Local Similarity Matches 48; Conser

Conservative

0;

41.0%;

Score 48; Pred. No. Mismatches

DB 23; 1.2e-42;

Length 118; Indels

0

Gaps

0

Query Match

Sequence

118 AA;

δÃ

70

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                                 Qy
                                                                                                                                B
                                                                     Matches
                                                                                              Query Match
                                                                                                                                                                The present sequence represents a protein that is selective towards heavy metal ions. It is used in the construction of the sensor of the invention. The specification describes a metal ion-specific, affinity sensor that measures capacitance. The sensor comprises a piece of noble metal to which are bound groups that bind specifically to selected heavy metal ions. These groups are bound to a self-assembling monolayer that covers at least 90% more preferably at least 99% of the noble metal surface. The noble metal is a rod or piece of insulating material glass, quartz or silica) on which a noble metal is sputtered. The sensor is used for qualitative or quantitative detection of selected heavy metal ions in liquid samples, particularly of zinc, mercury, cadmium, copper and lead in e.g. environmental samples, medicines, foods and other readmire.
                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                Claim 8; Page 22-23; 40pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                              Capacitance sensor specific for heavy metal ions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Berggren C, Bontidean I, H
Hobman J, Jakeman K, Johan
Van Der Lelie D, Wilson J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1999-254424/21.
                                                                                                                                                         foods and other products.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (CSOE/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Heavy metal ion selectivity; metal ion-specific affinity sensor; capacitance measurement; noble metal; self-assembling monolayer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      25-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    W09914597-A1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pseudomonas aeruginosa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           zinc; mercury; cadmium; copper; lead; environmental sample; medicine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MerR protein which has selectivity towards heavy metal ions.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAY01816 standard; protein; 144 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 UNBI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (BERG/) BERGGREN C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30~JUN-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (BONT/)
79 GTHCEEASSLAEHKLKDVREKMADLARME 107
                               59 GTHCEEASSLAEHKLKDVREKMADLARME 87
                                                                                Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EHKLKDVREKMADLARMETVLSELVCACHARKGNVSCPSAWSHPQFEK 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  EHKLKDVREKMADLARMETVLSELVCACHARKGNVSCPSAWSHPQFEK 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     JOHANSSON G.
MATTIASSON B.
UNIV BIRMINHAM SCHOOL BIOLOGICAL SCI.
VITO VLAAMSE INSTELLING TECHNOLOGISCH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BONTIDEAN I.
CSOEREGI E.
                                                                                                                               144 AA;
                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       97SE-0003315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     98WO-SE01638
                                                                           24.8%; Score 29;
100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             n I, Brown N,
Johansson G,
                                                                0;
                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Corbisier P, Csoeregi
Lloyd J, Mattiasson B;
                                                                             DB 20;
. 1.5e-2;
                                                                                         Length 144;
                                                             Indels
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AAR49668
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XX
                                                                                                                                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity
20-JUL-1999; 99EP-0114072.
18-FEB-2000; 2000EP-0103551.
                                     20-JUL-2000; 2000WO-EP06968.
                                                                                                                                        Bacteriophage particle; protein display; influenza haemagglutinin peptide.
                                                                                         WO200105950-A2.
                                                                                                                 Haemophilus influenzae
                                                                                                                                                                                                     08-MAY-2001 (first entry)
                                                                                                                                                                                                                                                        AAY97662 standard; peptide; 10
                                                                 25-JAN-2001.
                                                                                                                                                                            Influenza haemagglutinin peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mercury resistant control gene merR and shuttle vector - for enhanced expression of mercury resistance marker in transformed
                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                   The mercury resistance genes can be used as selectable markers when used to transform other bacteria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Page 2; 26pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1994-077131/10.
N-PSDB; AAQ58554.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAR49668 standard; Protein; 159 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Thiobacillus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (AKIT-) AKITA KEN.
(DOWA ) DOWA MINING CO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17-JAN-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               11-JAN-1994.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       JP06000083-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Thiobacillus ferrooxidans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Protein product of mercury resistance control gene merR(1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAR49668;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17-JAN-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       transformation; detection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Resistance; mercury; selectable marker; Thiobacillus ferrooxidans;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16-SEP-1994 (first entry)
                                                                                                                                                                                                                                                                                                                        109 VLSELVCACHARKGNVSCPLIASL 132
                                                                                                                                                                                                                                                                                                                                                31 VLSELVCACHARKGNVSCPLIASL 54
                                                                                                                                                                                                                                                                                                                                                                                                                            159 AA;
                                                                                                                                                                                                                                                                                                                                                                           Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    91JP-0018338
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100.0%; Pred. No.
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2.9e-17;
                                                                                                                                                                                                                                                                                                                                                                                               Length 159;
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The invention relates to a method for displaying a polypeptide/protein on the control of the polypeptide/protein to a unit of the protein coat of the polypeptide/protein to a unit of the protein coat of the bacteriophage particle. The attachment is via a disulfide bond to the bacteriophage particle. The attachment is via a disulfide bond to the bacteriophage particle. The polypeptide/protein and a cysteine coat of the bacteriophage particle. A collection of the bacteriophage particles of a bacteriophage particle. A collection of the bacteriophage particles of useful for obtaining a polypeptide/protein having a desired property, by screening the collection and/or selecting from a bacteriophage complexing to a target of interest. The method further involves contacting conditions. The methods easy creation and bacteriophage to the target of interest to by treating the complexes of target of interest and bacteriophages under creducing conditions. The methods easy creation and screening of large bacteriophage particles with the target of interest conditions. The methods easy creation and screening of large bacteriophage particles.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-147336/15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (MORP-) MORPHOSYS AG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 2; Page 33; 80pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    in the polypeptide and cysteine residues in coat -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Loehning C,
                                                                                                                                                                                                                                     adipositas; bulimia; wasting; cachexia; eating disorder; body weight disorder; weight loss; cancer; infectious disease; hypogonadism; Prader-Willi syndrome; Laurence-Moon-Biedl syndrome; hypothyroidism; diabetes; Cushing's syndrome; endocrine disorder; pastrointestinal disease; inflammatory bowel disease; gastrointestinal disease; inflammatory bowel disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                  13-JUN-2001; 2001WO-EP06713
                                                          20-DEC-2001.
                                                                                                  WO200196371-A2
                                                                                                                                                                                                 ulcerative colitis; anorexia nervosa; glycogen storage disease; lipid storage disease; lipoma; liposarcoma; heart disease; hypertension;
                                                                                                                                                                                                                                                                                                                                            Adipose protein; adp; obesity; transgenic animal; obesity;
                                                                                                                                                                                                                                                                                                                                                                                    Peptide STREP tag.
                                                                                                                                                                                                                                                                                                                                                                                                                            12-MAR-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAU80475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAU80475 standard; Peptide; 10 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              108 SAWSHPQFEK 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 SAWSHPQFEK 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                acquired immunodeficiency syndrome;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  8.5%; Score 10; DB 22;
100.0%; Pred. No. 0.0012;
tive 0; Mismatches 0
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                                                                                                                                                                                    AIDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0,
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CC polypeptide which regulates, causes or contributes to obesity in an CC animal or a human. The polynucleotides, proteins, ant-adp antibodies, CC modulators of adp activity, adp antisense nucleic acids, expression CC wectors, adp transgenic animals are useful in the diagnosis and CC treatment of obesity, adipositas, bulimia, wasting (cachexia), eating CC disorders and/or disorders of body weight/body mass, weight loss due to CC cancer or infectious diseases, genetic disorders associated with CC hypogonadism e.g. Prader-Willi syndrome, Laurence-Moon-Biedl syndrome, CC gastrointestinal diseases, inflammatory bowel disease, ulcerative CC colitis, and anorexia nervosa. They are also useful for treating CC disorders of body weight/mass e.g. glycogen storage diseases, and lipid CC compositions are also useful for treating heart disease, hypertension, CC and infertility and for treating conditions associated with under weight ce.g. enhancing or controlling fertility, controlling weight loss in CC acquired immunodeficiency syndrome (AIDS) or cancer patients. The CC present sequence is a peptide tag used in a fusion protein with an CC adap protein to facilitate purification
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Best Local S
Matches 10
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23-JUN-2000;
28-JUN-2000;
17-APR-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel nucleic acid encoding adipose polypeptide which regulates, causes or contributes to obesity, useful for treating obesity, heart disease, hypertension, infertility, and controlling weight loss in cancer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 1; Page 185; 188pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2002-106464/14.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Broenner G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
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                                                                                                                                                           Streptavidin; purification;
                                                                                                                                                                                                                                                                                                       AAW59212 standard; peptide; 8 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (DEVE-) DEVELOGEN AG
10-OCT-1996;
                              09-OCT-1997;
                                                                                              EP835934-A2
                                                                                                                           Synthetic.
                                                                                                                                                                                                          Streptavidin tagged peptide ligand #2.
                                                                                                                                                                                                                                            27-AUG-1998
                                                              15-APR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                     108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                      1 SAWSHPQFEK 10
                                                                                                                                                                                                                                                                                                                                                                                                                   SAWSHPQFEK 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     10 AA;
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; 2000EP-0113049.
; 2000US-214518P.
; 2001EP-0109537.
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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                                                                                                                                                                                                                                            (first entry)
                                                                                                                                                                             ligand; binding affinity; mutant; isolation;
                                                                                                                                                              recover;
96DE-1041876
                                97EP-0117504
                                                                                                                                                                                                                                                                                                                                                                                                                                                 8.5%; >--
100.0%; Pr
                                                                                                                                                            immobilise
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DB 23;
. 0.0012;
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Job time: 75 secs
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Matches 8; Conserv
                                                                                                                                                                                                                                                              AAW59211 and AAW59212 are ligands used in a method to assay binding affinity of streptavidin mutants. These mutants have a mutation within the amino acid (aa) region 44-53 of the wild-type protein show a higher binding affinity than the wild-type for peptide ligands that include the sequence of formula Trp-X-His-Pro-Gln-Phe-Y-Z where X = any aa; Y and Z are both Gly, or Y = Glu and Z = Arg or Lys. Recombinant streptavidin mutants can be used to isolate, purify and determine proteins or to determine/recover substances that contain streptavidin-binding groups. Such compounds may also be used to immobilise fusions on microtitre plates, microbeads or sensor chips.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Streptavidin mutants with higher binding affinity for peptide ligands - have mutation in amino acid region 44-53, used to isolate, purify or determine fusion proteins including these ligands
                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 10; Page 11; 21pp; German.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 1998-218868/20.
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                                                                                                               110 WSHPQFEK 117
                                                                         1 WSHPQFEK 8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Voss S;
                                                                                                                                                                                                                                 8 AA;
                                                                                                                                                6.8%; Score 8; DB 19; Latilarity 100.0%; Pred. No. 7.8e+05; Conservative 0; Mismatches 0;
                                                                                                                                                                                         Length 8;
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Result
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Maximum DB seq length: 2000000000
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  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score
                                                      Query
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117
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pir2:*
pir3:*
pir4:*
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DB
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T13958
T14270
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S37670
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from

Query Match 47.0%; Score 55; DB 2; Length 144; Best Local Similarity 100.0%; Pred. No. 4.2e-50; Matches 55; Conservative 0; Mismatches 0; Gaps 0;	RESULT 2 S51706 regulatory protein merR - Alcaligenes faecalis c:Species: Alcaligenes faecalis C:Species: Alcaligenes faecalis C:Date: 07-May-1995 #sequence_revision 01-Sep-1995 #text_change 20-Sep-1999 C:Accession: S51706 R:Osborn, A.M., Bruce, K.D.; Strike, P.; Ritchie, D.A. submitted to the EMBL Data Library, May 1994 A;Description: Sequence conservation between regulatory mercury resistance genes A;Reference number: S51703 A;Accession: S51706 A;Status: preliminary A;Molecule type: DNA A;Residues: 1-144 <osb> A;Cross-references: EMBL:Z33484; NID:g607038; PIDN:CAA83892.1; PID:g607039 C;Superfamily: transcription repressor glnR</osb>	A;Genome: plasmid A;Genome: plasmid C;Superfamily: transcription repressor glnR C;Superfamily: transcription repressor glnR C;Superfamily: transcription repressor glnR C;Superfamily: transcription repressor glnR Query Match Query Match Best Local Similarity 100.0%; pred. No. 4 2e-50; Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Matches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Mismatches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Mismatches 1; Mismatches 0; Indels 0; Gaps 0; Mismatches 1; Mismatches 0; Indels 0; Gaps 0; Mismatches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Mismatches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Mismatches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Mismatches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Mismatches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Mismatches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Mismatches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Mismatches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Mismatches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Mismatches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Mismatches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Mismatches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Mismatches 55; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Mismatches 55; Conservative 0; Mismatches 0; Mism	RESULT 1 S09527 regulatory protein merR - plasmid NR1 C;Species: plasmid NR1 C;Species: plasmid NR1 C;Species: plasmid NR1 C;Date: 19 Mar-1997 #sequence_revision 29-Aug-1997 #text_change 20-Sep-1999 C;Accession: S09527 R;Barrineau, P.; Gilbert, P.; Jackson, W.J.; Jones, C.S.; Summers, A.O.; Wisdom, J. Wol. Appl. Genet. 2, 601-619, 1984 A;Title: The DNA sequence of the mercury resistance operon of the IncFII plasmid A;Reference number: S07447; MUID:85159407; PMID:6530603 A;Accession: S09527 A;Molecule type: DNA A;Residues: 1-14 < CBAR> A;Residues: 1-14 < CBAR> A;Residues: 1-14 < CBAR> A;Residues: 1-14 < CBAR> A;Residues: EMBL:K03089; NID:g150389; PIDN:AAB59072.1; PID:g455296	6 5.1 198 2	ypoth procarbo	
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A;Cross-references: EMBL:Z33490; NID:g607153; PIDN:CAA83898.1; C;Superfamily: transcription repressor glnR
                                                                                                                                                                                      A; Reference number: S51703
A; Accession: S51749
                                                                                                                                                                                                                       A; Description: Sequence conservation between regulatory mercury resistance genes from me
                                                                                                                                                                                                                                                                                         regulatory protein merR - Pseudomonas fluorescens
C;Species: Pseudomonas fluorescens
C;Date: 07-May-1995 #sequence_revision 19-Oct-1995 #text_change 24-May-2001
C;Accession: S51749
                                                                                                                             A; Molecule type: DNA
A; Residues: 1-144 < OSB>
                                                                                                                                                                    A; Status: preliminary
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submitted to the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Molecule type: DNA
A; Residues: 1-144 < OSB>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  regulatory protein merR - Pseudomonas sp.
C;Species: Pseudomonas sp.
C;Date: 07-May-1995 #sequence_revision 19-Oct-1995 #text_change 20-Sep-1999
C;Accession: S51755
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A;Description: Sequence conservation between regulator
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C;Accession: S51720
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A; Accession: S51720
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      regulatory protein merR - Enterobacter aerogenes C; Species: Enterobacter aerogenes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Residues: 1-144 <OSB>
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Best Local :
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            Local Similarity les 29; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                     79
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                                                                                                                                                                                                                                                                       A.M.; Bruce,
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                                                                                                                                                                                                                                                  Bruce, K.D.; Strike, P.; Ritchie, D.A. EMBL Data Library, May 1994
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+ive 0; Mismatches
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100.0%; Pred. No.
      score 29; DB; Pred. No. 7.5
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Pred. No.
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                          DB 2; L, 7.5e-23;
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                                               Length 144;
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RESULT 8
S51705
regulatory protein merR - Klebsiella oxytoca
C;Species: Klebsiella oxytoca
C;Date: 07-May-1995 #sequence_revision 01-Sep-1995 #text_change 20-Sep-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            regulatory protein wer.
C/Species: Acinetobacter calcoaceticus
A/Variety: isolate SE11, isolate SE12
C:Date: 07-May-1995 #sequence_revision 01-Sep-1995 #text_change 20-Sep-1999
                                                                                                                                                                                                                                                                                                                                                 C; Superfamily: transcription repressor glnR
                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-151 < OSB>
                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Reference number: S51703
A; Accession: S51721
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         regulatory protein merR - Enterobacter cloacae C; Species: Enterobacter cloacae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Gene: merR C; Superfamily: transcription repressor glnR
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S51703
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          A; Description: Sequence conservation between regulatory mercury resistance genes from
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A; Residues: 1-151 <OSB>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Cross-references: EMBL:Z33483; NID:g607034; PIDN:CAA83891.1; PID:g607035
A;Experimental source: isolate SE12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A; Residues: 1-151 < OSO>
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Best Local :
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                                                                                                                                                                     109 VLSELVCACHARKGNVSCPLIASLQ 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             109 VLSELVCACHARKGNVSCPLIASLQ 133
                                                                                                                                                                                                               31 VLSELVCACHARKGNVSCPLIASLQ 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          31 VISELVCACHARKGNVSCPLIASIQ 55
                                                                                                                                                                                                                                                                                    Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             79 GTHCEEASSLAEHKLKDVREKMADLARME 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A.M.; Bruce, K.D.; Strike, P.; Ritchie, D.A.
                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
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                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL:Z33482; NID:g607032; PIDN:CAA83890.1; PID:g607033
ce: isolate SE11
                                                                                                                                                                                                                                                   21.4%; Jr
100.0%; Pr
0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     conservation between regulatory mercury resistance genes from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21.4%;
100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Acinetobacter calcoaceticus (isolate SE11 and SE12)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0,
                                                                                                                                                                                                                                                                                 Score 25;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 25;
Pred. No.
                                                                                                                                                                                                                                                            Mismatches
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                                                                                                                                                                                                                                                                               DB 2; L
1.2e-18;
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                                                                                                                                                                                                                                                                                                    Length 151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length 151;
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Accession: S51705

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A:Cross-references: EMBL:L03729; NID:g1019671; PIDN:AAA98396.1; PID:g154910
A:Experimental source: plasmid Rpl; transposon Tn5053
R:Kholodii, G.Y.; Mindlin, S.Z.; Bass, I.A.; Yurieva, O.V.; Minakhina, S.V.; Nikiforov, Mol. Microbiol. 17, 1189-1200, 1995
A:Title: Four genes, two ends, and a res region are involved in transposition of Tn5053
A:Reference number: S70140; MUID:96130850; PMID:8594337
A:Accession: S70142
                                                                                                                                                                                                                                                                              A;Status: preliminary; translation not shown A;Molecule type: DNA A;Residues: 1-144 <KHO>
                                                                                                                                                                                                                                                                                                                                                              A;Title: Tn5053, a mercury resistance transposon with integron's ends A;Reference number: S32795; MUID:93253772; PMID:8387603 A;Accession: S32798
                                                                                                                                                                                                                                                                                                                                                                                                                 R;Kholodii, G.Y.; Yurieva, O.V.; Lomovskaya, O.L.; Gorlenko, Z.M.; Mindlin, J. Mol. Biol. 230, 1103-1107, 1993
A;Title: Tn5053, a mercury resistance transposon with integron's ends.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Species: Xanthomonas sp.
C;Date: 08-Dec-1993 #sequence_revision 01-Dec-1995 #text_change 20-Sep-1999
C;Accession: S32798; S70142
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R;Hobman, J.; Kholodii, G.; Nikiforov, V.; Ritchie, D.A.; Strike, P.; Yurieva, Gene 146, 73-78, 1994
A;Title: The sequence of the mer operon of pMER327/419 and transposon ends of A;Reference number: 139574; MUID:94341572; PMID:8063107
A;Accession: I39574
           A; Molecule type: DNA
A; Residues: 1-144 < K
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        C;Species: Alcaligenes sp.
C;Date: 19-Jul-1996 #sequence_revision 19-Jul-1996 #text_change 20-Sep-1999
C;Accession: I39574; S37035
                                                   A; Status: preliminary; nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 merR protein - Xanthomonas sp. transposon Tn5053
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C; Superfamily: transcription repressor glnR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Molecule type: DNA
A; Residues: 1-144 < RES>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R;Osborn, A.M.; Bruce, K.D.; Strike, P.; Ritchie, D.A. submitted to the EMBL Data Library, May 1994
A;Description: Sequence conservation between regulatory mercury resistance genes from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Cross-references: EMBL:Z23094; GB:L20693; NID:g388553; PIDN:AAB05979.1; PID:g388554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Status: preliminary; translated from GB/EMBL/DDBJ
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A; Residues: 1-151 < OSB>
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A;Accession: S51705
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%;
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Pred. No.
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1.6e-15;
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1.2e-18;
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                                                        RESULT
S51707
C; Species:
                               regulatory
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                                  ζ.
                                                                                                                                              C; Superfamily: transcription repressor glnR
                                                                                                                                                                                   A; Molecule type: DNA
A; Residues: 1-144 < HOB>
                                                                                                                                                                                                                                         A; Reference number: A; Accession: S37044
                                                                                                                                                                                                                                                        A; Description: The nucleotide sequence of the mer operon of pMJ100 and transposon end A; Reference number: {\bf S37035}
                                                                                                                                                                                                                                                                                                                                             C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 20-Sep-1999
                                                                                                                                                                                                                                                                                                                                                                    N;Alternate names: mer operon regulator C;Species: Pseudomonas fluorescens
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Gene: merR
A;Mobile element: transposon
C;Superfamily: transcription
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Cross-references: EMBL:L40585; NID:g710572; PIDN:AAA98322.1; PID:g710575 A;Note: the nucleotide sequence was submitted to the EMBL Data Library, May C;Genetics:
                                                                                                                                                              A; Cross-references: EMBL: Z23095; NID: g397617; PIDN: CAA80641.1;
                                                                                                                                                                                                                     A; Status: preliminary
                                                                                                                                                                                                                                                                                             submitted to the EMBL Data Library, June
                                                                                                                                                                                                                                                                                                                  R; Hobman,
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A; Accession: S51756
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A; Residues: 1-144 < OSB>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 submitted to the EMBL Data Library, May 1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C; Accession:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Date: 07-May-1995 #sequence_revision 10-Nov-1995 #text_change 20-Sep-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C; Species:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          regulatory protein merR - Comamonas testosteroni
C;Species: Comamonas testosteroni
                                                                                          Query Match
Best Local
                                                                         Matches
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113 LVCACHARKGNVSCPLIASLQG 134
                                  35 LVCACHARKGNVSCPLIASLQG 56
                                                                     Local Similarity es 22; Conserv
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22; Conserv
                                                                                                                                                                                                                                                                                                              Kholodii, G.; Nikiforov, V.; Ritchie, D.A.; Strike,
                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
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                                                                                        18.8%; Score 22; 100.0%; Pred. No.
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; Pred. No.
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; Pred. No.
                                                                         Mismatches
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protein merR - Agrobacterium Agrobacterium radiobacter

radiobacter

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R;Osborn, A.M.; Bruce, K.D.; Strike, P.; Ritchie, D.A. submitted to the EMBL Data Library, May 1994
A;Description: Sequence conservation between regulatory mercury resistance genes from me A;Reference number: S51703
A;Accession: S51707
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C;Accession: S51707
                                                                                                                                                                                           , S.; Moule, S.; O'Gaora, P.
Nature 413, 848-852, 2001
A;Authors: Parry, C.; Quail, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.;
A;Title: Complete genome sequence of a multiple drug resistant Salmonella enterica serov
A;Reference number: AB0502; PMID:11677608
A;Accession: AE0971
                                                                                                                                                                                                                                                                                                                                                                                                                          50S ribosomal chain protein L28 [imported] - Salmonella enterica subsp. enterica Scrovar Typhi C;Species: Salmonella enterica subsp. enterica serovar Typhi A;Note: this species has also been called Salmonella typhi C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 17-May-2002 C;Accession: AE0971
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R;Nucifora, G.; Chu, L.; Silver, S.; Misra, T.K.
J. Bacteriol. 171, 4241-4247, 1989
A;Title: Mercury operon regulation by the merR gene of the organomercurial resistance A;Reference number: A33858; MUID:89327136; PMID:2666393
A;Accession: A33858
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C;Species: Escherichia coli
C;Date: 09-Mar-1990 #sequence_revision 09-Mar-1990 #text_change 20-Sep-1999
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C;Keywords: DNA binding; transcription regulation
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A;Molecule type: DNA
A;Residues: 1-144 < NUC>
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A;Molecule type: DNA
A;Residues: 1-151 <OSB>
A;Cross-references: GB:AL513382; PIDN:CAD03265.1; PID:g16504886; C;Genetics: A;Gene: ST44066
C;Superfamily: Escherichia coli ribosomal protein L28
                                                                                                                                                                                                                                                                                                                                        R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churcher, th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Farrar, S.; Moule, S.; O'Gaora, P.
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100.0%; Pred. No. 2.1e-13;
Live 0; Mismatches 0;
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Query Match 6.0%; Score 7; DB 2; Length 78;

Best Local Similarity 100.0%; Pred. No. 5.1;

Matches 7; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 87 ETVLSEL 93

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Db 65 ETVLSEL 71
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Search completed: May 28, 2003, 10:42:29
Job time: 45 secs

Result Minimum DB seq length: 0
Maximum DB seq length: 2000000000 Title: Perfect score: Database : Total number of hits satisfying chosen parameters: Word size : Scoring table: Sequence: OM protein - protein search, using sw Post-processing: Listing first 45 summaries on: 33210987554 33210987554 and is Score No. is the number of results predicted by chance to have a greater than or equal to the score of the result being printed, s derived by analysis of the total score distribution. US-09-977-137A-4 117 Match Query 112892 seqs, 41476328 residues OLIGO 1 MTHCEEASSLAEHKLKDVRE.... May 28, 2003, 10:29:42; Search time 24 Seconds Gapop 60.0 , Gapext 60.0 0 12247 66.000 66.000 66.000 66.000 66.000 66.000 66.000 66.000 66.000 66.000 66.000 66.000 66.000 66.000 SwissProt_40:* GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd. Length DB EFP_IACLA
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SH3B_MOUSE
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202.197 Million cell updates/sec P07044 salmonella
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2 pseudanabae
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Matches 55
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01-JAN-1988
15-DEC-1998
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"Mutagenesis of the cysteines in the metalloregulatory protein MerR indicates that a metal-bridged dimer activates transcription.";
Biochemistry 28:6140-6145(1989).
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SMART; SMO0422; HTH_MERR; 1.
PROSITE; PSO0552; HTH_MERR FAMILY; 1.
Transcription regulation; Activator; Repressor; Mercuric resistance;
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TRANSPOSON-Fn501;
TRANSPOSON-Fn501;
PubMed-6091128;
MISTA T.K., Brown N.L., Fritzinger D.C., Pridmore R.D.,
Barnes W.M., Haberstroh L., Silver S.;
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                                                                                                                                                                                                                                                                                                                                                                                                     MUTAGENESIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Osborn A.M., Bruce K.D., Strike P., Ritchie D.A.; Submitted (DEC-1994) to the EMBL/GenBank/DDBJ databases.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "Mercuric ion-resistance operons of plasmid R100 mn501: the beginning of the operon including the and the first two structural genes."; Proc. Natl. Acad. Sci. U.S.A. 81:5975-5979(1984).
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                                                                                          SIMILARITY:
                                                                                                                                   RESISTANCE OPERON. IN THE ABSENCE OF MERCURY MERR REPRESSES TRANSCRIPTION BY BINDING TIGHTLY TO THE MER OPERATOR REGION; WHEN MERCURY IS PRESENT THE DIMERIC COMPLEX BINDS A SINGLE ION AND BECOMES A POTENT TRANSCRIPTIONAL ACTIVATOR, WHILE REMAINING
                                                                        REGULATORS.
                                                                                                                      BOUND TO THE MER SITE
                                                                                                                                                                                                                                               FUNCTION: MEDIATES THE MERCURIC-DEPENDENT INDUCTION OF MERCURY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    THCEEASSLAEHKLKDVREKMADLARMETVLSELVCACHARKGNVSCPLIASLQG 134
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AL513383; CAD09817.1; -.
K03089; AAB59072.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (Rel. 06, Created)
(Rel. 06, Last sequence update)
(Rel. 37, Last annotation update)
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                                                                                               BELONGS
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                                                                                          TO THE MERR FAMILY OF TRANSCRIPTIONAL
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Pred. No.
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HG(2+)
HG(2+)
HG(2+).
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MERR_SERMA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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                                                                                                                                                                                                   NUCLIFORA G., Chu L., SILVER S., MISRA T.K.;

"MERCURY Operon regulation by the merr gene of the organomercurial resistance system of plasmid pDU1358.";

J. Bacteriol. 171:4241-4247 (1989).

-!- FUNCTION: MEDIATES THE MERCURIC-DEPENDENT INDUCTION OF MERCURY RESISTANCE OPERON. IN THE ABSENCE OF MERCURY MERR REPRESSES TRANSCRIPTION BY BINDING TIGHTLY TO THE MER OPERATOR REGION;
WHEN MERCURY IS PRESENT THE DIMERIC COMPLEX BINDS A SINGLE ION AND BECOMES A POTENT TRANSCRIPTIONAL ACTIVATOR, WHILE REMAINING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
01-OCT-1993 (Rel. 27, Last annotation update)
Mercuric resistance operon regulatory protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PROSITE; PS00552; HTH_MERR_FAMILY; 1.

Transcription regulation; Activator; Repressor; Mercuric Mercury; DNA-binding; Plasmid; Transposable element.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; Z00027; CAA77320.1; -. EMBL; Z33489; CAA83897.1; -. EMBL; Z33490; CAA83898.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=89327136; PubMed=2666393;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Serratia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Plasmid pDU1358
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Serratia marcescens.
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Pfam; PF00376; merR; 1.
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                                                                                                                              REGULATORS.
                                                                                                                                                      BOUND TO THE MER SITE.
SIMILARITY: BELONGS TO THE MERR FAMILY OF TRANSCRIPTIONAL
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HG(2+).
HG(2+).
C->A: ABOLISHES TRANSCRIPTIONAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           C->A: SLIGHT INCREASE IN TRANSCRIPTIONAL ACTIVATION.
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C573298AFF0846EF CRC64;
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Pfam; PF00376; merR; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                         SPECIES-S.typhimurium; STRAIN-LTZ:
MEDLINE-98055334; PubMed-9393616;
Suzuki M., Matsui K., Yamada M., Kasai H., Sofuni T., Nohmi T.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
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PROSITE; PS00552; HTH_MERR_FAMILY; 1.
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SPECIES-S.typhi; STRAIN-CT18;
MEDLINE-21534947; PubMed-11677608;
Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.
Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia M.,
Baker S., Basham D., Brooks K., Chillingworth T., Connerton P.,
Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,
Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K.,
Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,
                                                                                                                                                                                                                 McClelland M., Sanderson K.E., Spieth J., Clifton S.W., Latreille P., Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S., Layman D., Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mulvaney E., Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan M.,
                                                                                                                                                                                                                                                                             SPECIES-S.typhimurium; STRAIN-LT2 / SGSC1412 / ATCC 700720; MEDLINE-21534948; PubMed-11677609;
                                                                                                                                                                                                                                                                                                                                            "Construction of mutants of Salmonella typhimurium deficient in 8-hydroxyguanine DNA glycosylase and their sensitivities to oxidative mutagens and nitro compounds.";
Mutat. Res. 393:233-246(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Salmonella typhimurium, and
Salmonella typhi
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
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15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RL28_SALTY
                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                      Waterston R.,
                                                                                                                                                          Nature 413:852-856(2001).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GTHCEEASSLAEHKL 73
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           144 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           126
                                                                                                                                                                                                   Wilson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  HTHMERR.
                                                                                                                                                                                       sequence of Salmonella enterica serovar Typhimurium
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                                                                                                                                                                                                      R.K.;
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HG(2+).
HG(2+).
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Pred. No.
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RESULT 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Complete genome sequence of a multiple drug resistant Salmonella enterica serovar Typhi CT18.";
Nature 413:848-852(2001).
-!- SIMILARITY: BELONGS TO THE L28P FAMILY OF RIBOSOMAL PROTEINS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Quail M., Rutherford K., Simmonds M., Skelton J., Stevens K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                         TRAD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; U23405; AAC01771.1; -. EMBL; AE008873; AAL22587.1; -. EMBL; AL627280; CAD03265.1; -.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Whitehead S., Barrell B.G.;
                                                                                                                                                                                                                                                      Miele L., Strack B., Kruft V., Lanka E.; "Gene organization and nucleotide sequence of the primase region IncP plasmids RP4 and R751.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-AUG-1992 (Rel.
01-AUG-1992 (Rel.
15-JUN-2002 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TRD5_ECOLI P27192;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ribosomal protein; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Pfam; PF00830; Ribosomal_L28; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   StyGene; SG10696; rpmB.
InterPro; IPR001383; Ribosomal_L28.
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                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its
                                                                                                                                                                                                                                                                                                                                                                               Escherichia
                                                                                                                                                                                                                                                                                                                                                                                          Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                           Plasmid IncP-beta R751
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TIGRFAMS; TIGR00009; L28;
                                       entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                      use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                               Submitted (AUG-1996) to the EMBL/GenBank/DDBJ databases -i- SIMILARITY: TO PLASMID INCP-ALPHA RP4 TRAD.
                                                                                                                                                                                                                                                                                                                     STRAIN-HB101
                                                                                                                                                                                                                                                                                                                                                                                                                           Escherichia coli.
                                                                                                                                                                                             Thomas C.M.
                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=562;
                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                  MEDLINE=92297959; PubMed=1818755;
                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A., AND SEQUENCE OF 1-4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       64 ETVLSEL 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     87 ETVLSEL 93
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X59794; CAA42459.1;
U67194; AAC64471.1;
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                                                                                                                                                                                                                                           2:145-162(1991).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            77 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23, Last sequence update)
41, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23, Created)
23, Last seq
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100.0%; Pr
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                                                                                      rmatics Institute. There are no rest institutions as long as its content
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                                                                                                                                                                                                                                                                                       Lanka E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   129
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FLGI_RHIME
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Best Local
                                                      CONFLICT
                                                                                                                                                                                                                                                                                                                                                the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Capela D., Barloy-Hubler F., Gouzy J., Bothe G., Ampe F., Batut J. Botstard P., Becker A., Boutry M., Cadieu E., Dreano S., Gloux S., Godrie T., Goffeau A., Kahn D., Kiss E., Lelaure V., Masuy D., Pohl T., Portetelle D., Puehler A., Purnelle B., Ramsperger U., Renard C., Thebault P., Vandenbol M., Weidner S., Galibert F.; "Analysis of the chromosome sequence of the legume symbiont Sinorhizobium meliloti strain 1021.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sinorhizobium meliloti strain 1021.";
Proc. Natl. Acad. Sci. U.S.A. 98:9877-9882(2001).
-i- FUNCTION: ASSEMBLES AROUND THE ROD TO FORM THE L-RING AND PROBABLY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PIR; S37
Plasmid
        SEQUENCE
                                     CONFLICT
                                                                                                                        CHAIN
                                                                                                                                                                                                      PRINTS;
                                                                                                                                                                                                                          InterPro; IPR001782; Flag_FlgI.
Pfam; PF02119; FlgI; 1.
                                                                                                                                                                                                                                                                                   EMBL; L49337; AAB81415.1; -.
EMBL; AL591784; CAC45236.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-JUN-2002 (Rel. 41, Last annotation update)
Flagellar P-ring protein precursor (Basal body P-ring protein).
FLGI OR R00664 OR SMC03012.
Rhizobium meliloti (Sinorhizobium meliloti).
Bacteria: Proteobacteria; alpha subdivision; Rhizobiaceae group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (MAR-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-RU11/001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      15-JUN-2002 (Rel. 41, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FLGI_RHIME Q52948;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE=21396507; PubMed=11481430;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  01-NOV-1997
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBCELLULAR LOCATION: Periplasmic (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SIMILARITY: BELONGS TO THE FLGI FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FUNCTION: ASSEMBLES AROUND THE ROD TO FORM THE L-RING AND PROTECTS THE MOTOR/BASAL BODY FROM SHEARING FORCES DURING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         S37670; S37670.
                                                                                                                                                                                                PR01010; FLGPRINGFLGI.
                                                                                                                                                                         Periplasmic;
  323
371 AA;
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     38357 MW;
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100.0%; Pred. No.
                                                                                                                                                                      Signal;
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                            FLAGELLAR P-RING PROTEIN
N -> K (IN REF. 1).
V -> A (IN REF. 1).
G -> GR (IN REF. 1).
                                                                                                                                       POTENTIAL.
06BB4E95EE029100 CRC64;
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Best Local Similarity
7; Conserve
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                                                                                                                                                                                       Matches
                                                                                                                                                                                                  Query Match
Best Local
                    01-APR-1990 (Rel. 14, Created)
01-OCT-1994 (Rel. 30, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
C-Rel proto-oncogene protein (C-Rel protein).
                                                                   REL_MOUSE
P15307;
                                                                                                                                                                                                                                                                                                                                                                                                                    entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                       InterPro; IPR00669; Mannitol_dh.
Pfam; PF01232; Mannitol_dh; 1.
PRINTS; PR00084; MTLDHDRGNASE; FALSE_NEG
PROSITE; PS00974; MANNITOL_DHGENASE; FALSE_NEG
                                                                                                                                                                                                                                                                                                                                                   the European Bioinformatics Institute. There are no rest
use by non-profit institutions as long as its content
modified and this statement is not removed. Usage by ar
                                                                                                                                                                                                                                           Oxidoreductase;
                                                                                                                                                                                                                                                                                                        EMBL; AL646068; CAD15836.1; -.
                                                                                                                                                                                                                                                                                                                                                                                   This SWISS PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ralstonia solanacearum (Pseudomonas solanacearum).
Bacteria; Proteobacteria; beta subdivision; Ralstonia group;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DALD_RALSO P58708;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             D-arabinitol
                                                                                                                                          203
                                                                                                                                                                103 NVSCPSA 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=21681879; PubMed=11823852;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=305;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ralstonia
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-JUN-2002 (Rel. 41, Last sequence update)
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                                                                                                                                                                                                Local
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                                                                                                                                         NVSCPSA 209
                                                                                                                                                                                       Similarity
7; Conser
                                                                                                                                                                                                                                    465 AA;
                                                                                                                                                                                       Conservative
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4-dehydrogenase (EC 1.1.1.11).
                                                                               STANDARD;
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50630 MW; 47095425D4836342 CRC64;
                                                                                                                                                                                                6.0%;
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100.0%; Pred. No.
tive 0; Mismatc
                                                                                                                                                                                              Score 7; ; Pred. No.
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                                                                                                                                                                                     Mismatches
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                                                                               587
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o. 8.5;
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                                                                               B
                                                                                                                                                                                                          Length 465;
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REL.

Mus musculus (Mouse).

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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                               PHA2_PSEA9 STANDARD;
Q52452;
Q1.NOV-1997 (Rel. 35, Created)
01.NOV-1997 (Rel. 35, Last seq
01.NOV-1997 (Rel. 35, Last ann
C-phycocyanin-2 alpha chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Grumont R.J., Gerondakis S.;
"The murine c-rel proto-oncogene encodes two mRNAs the expression of which is modulated by lymphoid stimuli.";
Oncogene Res. 5:245-254(1990).
-I- FUNCTION: PROTO-ONCOGENE THAT MAY PLAY A ROLE IN DIFFERENTIATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Grumont R.J., Gerondakis S.; "Structure of a mammalian c-rel protein deduced from the nucleotide sequence of murine cDNA clones.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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STRAIN=BALB/c; TISSUE=Spleen;
MEDLINE=89239482; PubMed=2654811;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR002909; IPT_TIG.
InterPro; IPR00451; NF_Rel_dor_fam.
Pfam; PF00554; RHD; 1.
Pfam; PF01833; TIG; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PIR; A45505; A45505.
PIR; A60367; A60367.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EMBL; X15842; CAA33843.1; ALT_SEQ. EMBL; X60271; CAA42817.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  modified and this statement is not removed.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PROSITE; PS01204; REL_1; 1.

PROSITE; PS50254; REL_2; 1.

Proto-oncogene; Phosphorylation; Nuclear protein.

DOMAIN 8 297 REL-LIKE (RHD).
                                                  Pseudanabaena sp.
                                                                               CPCA2
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MGD; MGI:97897; Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HSSP; P25799; 1BFT
NCBI_TaxID=29415;
                          Bacteria; Cyanobacteria; Oscillatoriales; Pseudanabaena
                                                                                                                                                                                                                                                                                                                                                          440
                                                                                                                                                                                                                                                                                                                                                                                                       24 DLARMET 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Local
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SIMILARITY: BELONGS TO THE REL/DORSAL FAMILY.
                                                                                                                                                                                                                                                                                                                                                          DLARMET 446
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SM00429; IPT; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity 7; Conser
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267
587 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                       . 35, Created)
. 35, Last sequ
. 35, Last anno
                                                  (strain PCC 7409)
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                                                                                                                            Last sequence update)
Last annotation updat
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUCLEAR LOCALIZATION SIGNAL (POTENTIAL).
PHOSPHORYLATION (BY PKA) (POTENTIAL).
98FC237B6D140416 CRC64;
                                                                                                                                                                                                                                 PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mismatches
                                                                                                                                                                                                                                   162 AA
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PHA3_FREDI
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Best Local :
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P14876;
01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last seque
01-JUL-1993 (Rel. 26, Last annot
C-phycocyanin-3 alpha chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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HSSP; P07122; 1CPC.
InterPro; IPR001659; Phycobilisome.
the European Bioinformatics Institute. There are no rest
use by non-profit institutions as long as its content
modified and this statement is not removed. Usage by ar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mazel D., Houmard J., Tandeau de Marsac N.;
"A multigene family in Calothax sp. PCC 7601 encodes phycocyanin, the major component of the cyanobacterial light harvesting antenna.";
Mol. Gen. Genet. 211:296-304(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fremyella diplosiphon (Calothrix PCC 7601).
Bacteria; Cyanobacteria; Nostocales; Rivulariaceae; Fremyella.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Multigene family.
BINDING 84
SEQUENCE 162 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Pfam; PF00502; Phycobilisome; 1.
ProDom; PD000340; Phycobilisome; 1.
Phycobilisome; Electron transport; Photosynthesis; Bile pigment;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the European Bioinformatics Institute. The surple of the second of the s
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                                                                                                                                                                                                                                          FROM THE PHYCOBILIPROTEIN COMPLEX.

-!- SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA CHAIN.
-!- INDUCTION: PHYCOCYANIN-3 IS EXPRESSED IN RED LIGHT UNDER CONDITIONS OF SULFUR DEPRIVATION.
-!- PTM: CONTAINS ONE COVALENTLY LINKED BILIN CHROMOPHORE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mazel D., Marilere P.;
"Adaptive eradication of methionine and cysteine from cyanobacterial light-harvesting proteins.";
Nature 341:245-248(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A. MEDLINE=89384903; PubMed=2506452;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CPCA3
                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- FUNCTION: LIGHT-HARVESTING PHOTOSYNTHETIC BILE PIGMENT-PROTEIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    48 ASSLAE 53
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Last annotation updat
chain.
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BILE PIGMENT-PROTEIN
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  Query Match
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HPRT_VIBHA

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P18134;

O1-NOV-1990 (Rel. 16, Created)

O1-NOV-1990 (Rel. 16, Last sequence update)

15-JUN-2002 (Rel. 41, Last annotation update)

16-Yanthine phosphoribosyltransferase (EC 2.4.2.8) (HPRT).
                                                                                                                               InterPro; IPR000836; PRTransferase.
InterPro; IPR002375; Pr/py_rp_transf.
Pfam; PF00156; Pribosyltran; 1.
TIGREAMS; TIGR01203; HGPRTase; 1.
PROSITE; PS00103; PUR_PYR_PR_TRANSFER; 1.
Transferase; Glycosyltransferase; Purine salvage; Magnesium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                        the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                   EMBL; X53382; CAA37462.1; -. PIR; S10993; S10993. HSSP; Q26997; 1QK3.
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PIR; S05712; S05712.
HSSP; P07122; ICPC.
InterPro; IPR001659; Phycobilisome.
Pfam; PF00502; Phycobilisome; 1.
ProDom; PD000340; Phycobilisome; 1.
                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                   or send an email to license@isb-sib.ch).
                                                                                                                   METAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            <del>-</del>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Showalter R.E., Silverman M.R.; nucleotide sequence of a gene, hpt, for hypoxanthine phosphoribosyltransferase from Vibrio harveyi.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Vibrio harveyi.
Bacteria; Proteobacteria; gamma subdivision; Vibrionaceae; Vibrio.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Phycobilisome; Electron transport; Photosynthesis; Bile pigment; Multigene family.
BINDING 84 84 PHYCOCYANOBILIN CHROMOPHORE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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SIMILARITY: BELONGS TO THE PURINE/PYRIMIDINE PHOSPHORIBOSYLTRANSFERASE FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              alpha-D-ribose 1-diphosphate.
PATHWAY: Purine salvage.
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                                                           ÀΑ;
                                                           19963 MW;
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17392 MW;
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                                                                            MAGNESIUM (BY SIMILARITY).
MAGNESIUM (BY SIMILARITY).
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Score 6;
                                                     2027D73A9CAAAACE CRC64;
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Length 176;

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Best Local (
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                                                                                                                                          _LACLA
                         Q9CHN6;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Elongation factor P (EF-P).
EFP OR LL0692.
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IF3C_GALSU
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16-OCT-2001
16-OCT-2001
16-OCT-2001
 Lactococcus lactis (subsp. lactis) (Streptococcus lactis). Bacteria; Firmicutes; Lactobacillales; Streptococcaceae; L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.

-I- FUNCTION: IF-3 BINDS TO THE 308 RIBOSOMAL SUBUNIT AND SHIFTS THE EQUILIBRUM BETWEEN 708 RIBOSOMES AND THEIR 508 AND 308 SUBUNITS IN FAYOR OF THE FREE SUBUNITS, THUS ENHANCING THE AVAILABILITY OF 308 SUBUNITS ON WHICH PROTEIN SYNTHESIS INITIATION BEGINS.
                                                                                                                            EFP_LACLA
                                                                                                                                                                                                                                                                                                                                                            Pfam; PF00707; IF3; 1.
ProDom; PD002880; IF3; 1.
TIGRFAMS; TIGR00168; infC; 1.
PROSITE; PS00938; IF3; 1.
                                                                                                                                                                                                                                                                                                                               Initiation factor; Protein biosynthesis; Chloroplast SEQUENCE 181 AA; 21393 MW; 572014236DE7ABF8 CRC6
                                                                                                                                                                                                                                                                                                                                                                                                        InterPro; IPR001288; IF3. Pfam; PF00707; IF3; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AF233069; AAF81685.1; -. HSSP; P03000; lTIF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-UTEX 2393; Whitney S.M., And
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Galdieria sulphuraria Chloroplast
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16-OCT-2001 (Rel. 40, 1
16-OCT-2001 (Rel. 40, 1
Translation initiation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=130081;
                                                                                                                                                                                                        156 SSLAEH 161
                                                                                                                                                                                                                                      66 SSLAEH 71
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBUNIT: MONOMER (BY SIMILARITY).
SUBCELLULAR LOCATION: Chloroplast.
SIMILARITY: BELONGS TO THE IF-3 FAMILY.
                                                                                                                                                                                                                                                                    Similarity 6; Conserv
                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Andrews J.;
                                                                                                                          STANDARD;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              40, Created)
40, Last sequence update)
40, Last sequence update)
40, Last annotation update)
ation factor IF-3, chloroplast.
                                                                                                                                                                                                                                                                                 100.0%;
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                                                                                                                                                                                                                                                                 %; Score 6; DB 1
%; Pred. No. 43;
0; Mismatches
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0; Mismatches
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                                                                                                                            185 AA
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                                                                                                                                                                                                                                                                                               Length 181;
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Lactococcus
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NCBI_TaxID=1360;

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RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               lactis ssp. lactis IL1463.";
Genome Res. 11:731-753(2001).
-1- FUNCTION: INVOLVED IN PEPTIDE BOND SYNTHESIS. STIMULATES EFFICIENT TRANSLATION AND PEPTIDE-BOND SYNTHESIS ON NATIVE OR RECONSTITUTED 70S RIBOSOMES IN VITRO. PROBABLY FUNCTIONS INDIRECTLY BY ALTERING THE AFFINITY OF THE RIBOSOME FOR AMINOACYL-TRNA, THUS INCREASING
                                                                                                   "Sequence analysis and interposon mutagenesis of a sensor-kinase (DctS) and response-regulator (DctR) controlling synthesis of the high-affinity C4-dicarboxylate transport system in Rhodobacter capsulatus.";
                                                                                                                                                                                       SEQUENCE FROM N.A.
STRAIN-ATCC 33303 / B10;
MEDLINE-93204897; PubMed-8455557;
                                                                                                                                                                                                                                                                                                                                                                 01-OCT-1994 (Rel. 30, Created)
01-OCT-1994 (Rel. 30, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro; IPR001059; EF-P.
Pfam; PF01132; EFF; 1.
TIGRFAMs; TIGR00038; efp; 1.
PROSITE; PS01275; EFP; 1.
Protein biosynthesis; Elongation factor; Complete proteome.
Protein biosynthesis; Blongation factor; Complete proteome.
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                                                                                                                                                                                                                                                                                   Rhodobacter
                                                                                                                                                                                                                                                                                              Rhodobacter capsulatus (Rhodopseudomonas capsulata).
Bacteria; Proteobacteria; alpha subdivision; Rhodobacter group;
                                                                                                                                                                                                                                                                                                                                                   C4-dicarboxylate transport transcriptional regulatory protein dctR.
                                                                                                                                                                                                                                                                                                                                                                                                                       P37740;
                                                                                                                                                                                                                                                                                                                                                                                                                                          DCTR_RHOCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bolotin A., Wincker P., Mauger S., Jaillon O., Malarme K., Weissenbach J., Ehrlich S.D., Sorokin A.;
                                                                                                                                                                                                                                                               NCBI_TaxID=1061;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AE006302; AAK04790.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=21235186; PubMed=11337471;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14 KLKDVR 19
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
                                                  FUNCTION: MEMBER OF THE TWO-COMPONENT REGULATORY SYSTEM DCTS/DCTR INVOLVED IN THE TRANSPORT OF C4-DICARBOXYLATES. DCTR FUNCTIONS AS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SUBCELLULAR LOCATION: Cytoplasmic.
SIMILARITY: BELONGS TO THE ELONGATION FACTOR P FAMILY.
                  A TRANSCRIPTIONAL REPRESSOR OF GENES TRANSPORT.
SUBCELLULAR LOCATION: Cytoplasmic (Probable)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PATHWAY: Protein biosynthesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    THEIR REACTIVITY AS ACCEPTORS FOR PEPTIDYL TRANSFERASE (BY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complete genome sequence of the lactic acid bacterium Lactococcus
                                                                                       Gen. Genet. 237:215-224(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                6;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                          STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  5.1%;
100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                        197 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    43;
                                  FOR C4-DICARBOXYLATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
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RNH2_MAGSA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local
                                                                                                           Matsunaga T., Submitted (JUL-1994) to the EMBL/GenBank/DDBJ databases. Submitted (JUL-1994) to the EMBL/GenBank/DDBJ databases. In FUNCTION: THIS ENZYME IS AN ENDONICLEASE THAT DEGRADES RNA-DNA HYBRIDS SPECIFICALLY (BY SIMILARITY).

-i- CATALYTIC ACTIVITY: Endonucleolytic cleavage to 5'-
                                                                                                                                                                                                                                                                                                                             RNH2_MAGSA STANDARD;

Q50412;

16-OCT-2001 (Rel. 40, Created)

16-OCT-2001 (Rel. 40, Last seq

16-OCT-2001 (Rel. 40, Last ann
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA_BIND
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PROSITE; PS00622; HTH_LUXR_FAMILY; 1. PROSITE; PS50110; RESPONSE_REGULATORY; Sensory transduction; Phosphorylation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRINTS; PR00038; HTHLUXR.
ProDom; PD000039; Response_reg;
ProDom; PD000307; HTH_LUXR; 1.
SMART; SM00421; HTH_LUXR; 1.
SMART; SM00448; REC; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR001789; Response_r
pfam; pF00072; response_reg; 1.
pfam; pF00196; GerE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                    RNHB.
                                                                                                                                                                                                                                                                                                               Ribonuclease
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Activator; DNA-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PIR; S30289; S30289.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; X64733; CAA46000.1; -.
                                                         -!- SUBCELLULAR LOCATION: Cytoplasmic (Potential).
                                                                                                                                                                                              STRAIN=AMB-1;
                                                                                                                                                                                                                                        NCBI_TaxID=84159;
                                                                                                                                                                                                                                                         Magnetospirillum.
                                                                                                                                                                                                                                                                    Bacteria; Proteobacteria; alpha subdivision; Rhodospirillaceae,
                                                                                                                                                                                                                                                                                  Magnetospirillum sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DOMAIN
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                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   191 ADLARM 196
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 81 ADLARM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PTM: PHOSPHORYLATED BY DCTS
SIMILARITY: CONTAINS 1 RESPO
SIMILARITY: BELONGS TO THE
                                                                      phosphomonoester.
COFACTOR: MANGANESE (BY SIMILARITY)
SUBCELLULAR LOCATION: Cytoplasmic (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RES
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197 i
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ilarity 100.0%;
Conservative
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128
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                                                                                                                                                                                                                                                                                                              . 40, Last sequence update)
. 40, Last annotation updat
(EC 3.1.26.4) (RNase HII).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        21270 MW;
                                                                                                                                                                                                                                                                                     (strain AMB-1)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RESPONSE REGULATORY DOMAIN.
THE LUXR/UHPA FAMILY OF TRANSCRIPTIONAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 6;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     H-T-H MOTIF (BY SIMILARIT C5F72003FCACOAD4 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESPONSE REGULATORY.
PHOSPHORYLATION (BY SIMILARITY)
INTER-DOMAIN LINKER (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             _reg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                            201
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    Transcription regulation;

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                                                                                                                                                    THE RNA OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                0,
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European Bioinformatics

Institute.

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Result
No.
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                                                                                           Database
                                                                                                                                                                                                                                                                                                                                                                                                                             Post-processing: Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Word size :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Scoring table:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Title:
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                            Score
protein search, using sw
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11:
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                                                                                                                                                            Match
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                                                                                                                                                                       Query
SPTREMBL_21:*
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                        sp_phage: *
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sp_rvirus:*
sp_bacteriap:*
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144
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172
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Q44190
Q46655
Q9R9X0
Q52395
Q9AFK4
Q57492
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Q934S8
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Q57106
                                                                                                                                                            Ħ
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                                                                                                                                                                                        SUMMARIES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             671580
               08rk29 pseudomonas
044190 alcaligenes
046655 enterobacte
09r9x0 pseudomonas
052395 pseudomonas
09afk4 shigella fl
057492 enterobacte
007304 pseudomonas
057106 accinetobact
09r9w9 pseudomonas
060233 alcaligenes
093488 thiobactlu
044191 agrobacteri
09393 acinetobact
                                                                                                                                                             Description
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45	44	43	42	41	40	39	38	37	36	35 5	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17
o	6	6	6	6	σ	o	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	7	13	13	15
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Q8WH74	019129	Q9KNH0	030342	Q69007	P82126	004137	Q53840	P74440	Q9VBU7	Q9QUH6	Q9ESK6	Q9QX02	Q9UGE2	Q9QX12	Q9ET81	д9усв8	Q8TCS2	Q9SAK7	Q97ID5	Q8W4L8	Q9M2K7	Q9D511	Q9HH01	Q9Y9H7	Q975Q0	Q99092	054316	P77071
Q8wn/4 frasera tub	bos tau	0	<	7 human	sus sc	~	$\boldsymbol{\pi}$	P74440 synechocyst	Q9vbu7 drosophila	Q9quh6 rattus norv		Q9qx02 rattus norv	Q9uge2 homo sapien	N	Q9et81 rattus norv	Q9vcb8 drosophila		Q9sak7 arabidopsis					Q9hh01 pyrococcus	09y9h7 aeropyrum p	Q975q0 sulfolobus	D)	054316 thiobacillu	

ALIGNMENTS

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RESULT 2
Q44190
ID Q441
AC Q441
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                                                                                                                    Matches
                                                                                                                                       Query Match
 Q44190
Q44190;
                                                                                                                                                                                                                                                                                                                                                                    Q8RK29;
01-JUN-2002 (TrEMBLrel. 21,
01-JUN-2002 (TrEMBLrel. 21,
01-JUN-2002 (TrEMBLrel. 21,
                                                                                                                                                                                                                                TRANSPOSON-TN21 HOMOLOGUE;
Kholodii G.Y., Gorlenko Z.M., Mindlin S.Z., Nikiforov V.G.;
"Distribution of distinct microvariants of Tn5041 in environmental
                                                                                                                                                                                                                                                                                                                                                                                                                       Q8RK29
                                                                                                                                                                                                                                                                                                                                                              MerR protein (Fragment).
                                                                                                                                                                SEQUENCE
                                                                                                                                                                             NON_TER
                                                                                                                                                                                     Plasmid.
                                                                                                                                                                                               EMBL; AJ422225; CAD19592.1;
                                                                                                                                                                                                              Submitted (DEC-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
                                                                                                                                                                                                                                                                                                                           Plasmid pKLH22.
                                                                                                                                                                                                                                                                                                                                       Pseudomonas fluorescens.
                                                                                                                                                                                                                                                                                                                                                    MERR
                                                                                                                                                                                                                        bacteria.
                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                           NCBI_TaxID=294;
                                                                     Local Similarity
                                                                                            2 THCEEASSLAEHKLKDVREKMADLARMETVLSELVCACHARKGNVSCPLIASLQG
                                                                                                                                                                124 AA;
                                                                                                                   47.0%; Score 55; DB 2; Li
ilarity 100.0%; Pred. No. 1.8e-50;
Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                       PRELIMINARY;
              PRELIMINARY;
                                                                                                                                                                13759 MW;
                                                                                                                                                                                                                                                                                                                                                                         Created)
Last sequence update)
Last annotation update)
               PRT;
                                                                                                                                                                 C514222BB0ED7754 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                        124
               144 AA
                                                                                                                                                                                                                                                                                                                                                                                                                        B
                                                                                                                                        Length 124;
                                                                                                                    Indels
                                                                                                                     0;
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099093

007300 pseudomonas

Q93515 salmonella

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RESULT 3
Q46655
ID Q466656
AC Q466
AC Q466
AC Q466
DT 01-1
DT 01-2
DT 01-2
DT 01-3
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                                                                                                                     Matches
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Q46655;
01-NOV-1996 (TrEMBLrel. 0
01-NOV-1996 (TrEMBLrel. C
01-DEC-2001 (TrEMBLrel. 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-T238;
OSborn A.M., Bruce K.D., Strike P., Ritchie D.A.;
OSborn A.M., Bruce K.D., Strike P., Ritchie D.A.;
"Sequence Conservation between Regulatory Mercury Resistance Genes
from Mercury Polluted and Pristine Environments.";
Submitted (MAY-1994) to the EMBL/GenBank/DDBJ databases.
-I- SIMILARITY: BELONGS TO THE MERR FAMILY OF TRANSCRIPTIONAL
                                                                                                                                                                                                                                               PRINTS; PRO0040; HTHMERR.
SMART; SM00422; HTH_MERR; 1.
PROSITE; PSO00552; HTH_MERR_FAMILY; 1.
DNA-binding; Transcription regulation.
SEQUENCE 144 AA; 15652 MW; 1D6E1F5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Osborn A.M., Bruce K.D., Strike P., Kilcuite J...., Osborn A.M., Bruce K.D., Strike P., Kilcuite J...., Regulatory Mercury Resistance "Sequence Conservation between Regulatory Mercury Resistance from Mercury Polluted and Pristine Environments.", Granmitted (MAY-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                              REGULATORS.
EMBL; Z33488; CAA83896.1; -.
InterPro; IPR000551; HTH_MerR.
Pfam; PF00376; merR; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Enterobacter aerogenes (Aerobacter aerogenes).
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRINTS; PRO0040; HTHMERR; 1.
SMART; SMO0422; HTH_MERR; 1.
PROSITE; PSO0552; HTH_MERR_FAMILY; 1.
DNA-binding; Transcription regulation
DNA-binding; Transcription Regulation
SEQUENCE 144 AA; 15832 MW; B71D7FE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=548;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Enterobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Regulatory protein.
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Pfam; PF00376; merk;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; Z33484; CAA83892.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NCBI_TaxID=511;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Alcaligenes
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Alcaligenes faecalis.
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   17 DVREKMADLARMETVLSELVCACHARKGNVSCPLIASLQG
                                                                                                                                                            Local
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                                                                                                                                                100.0%;
                                                                                                                                                                                          34.28;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HTH_MerR.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             subdivision; Alcaligenaceae;
                                                                                                              Mismatches
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. 2e-50;
                                                                                                                                                                                          DB 2;
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                                                                                                                                                                               Length 144;
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                                                                                                                  Indels
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   ALC CONTRACTOR OF THE PROPERTY OF THE PROPERTY
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                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
SPECIES-P. putida; PLASMID-PWW0;
Greated A., Lambertson L., Williams P.A., Thomas C.M.;
"Complete nucleotide sequence of IncP-9 plasmid pww0.";
"Complete nucleotide sequence of EncP-9 plasmid pww0.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-NOV-1996
01-NOV-1996
01-MAR-2002
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Q52395;
Proc.
                                                     "Mercuric ion-resistance operons of plasmid R100 and transposon the beginning of the operon including the regulatory region and first two structural genes.";
                                                                                                                                                                           Misra T.K., Brown N.L., Fritzinger D.C., Pridmore R.D., Haberstroh L., Silver S.;
                                                                                                                                                                                                                                               SPECIES=P.stutzeri; STRAIN=OX; PL
MEDLINE=85014891; PubMed=6091128;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pseudomonas putida, and Pseudomonas perfectomarina).
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Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AF092069; AAD52705.1; -.
TnterPro; IPR000551; HTH_MerR.
                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=303,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pseudomonas
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9R9X0;
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01-JUN-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bruce K.D., Lilley A.K., Bailey M.J.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-KT2440;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17 DVREKMADLARMETVLSELVCACHARKGNVSCPLI 51
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                              Natl. Acad. Sci. U.S.A. 81:5975-5979(1984)
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35; Conser
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(TrEMBLrel. 01, Last sequence update)
(TrEMBLrel. 20, Last annotation update)
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Pred. No.
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                                                                                                                                                                                                                                                                                         PLASMID-PPB;
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SMART; SM00422; HTH_MERR; 1.
PROSITE; PS00552; HTH_MERR_FAMILY; 1.
Plasmid; DNA-binding; Transcription regulation.
Plasmid; DNA-binding; Transcription regulation.
SEQUENCE 144 AA; 15884 MW; F5760BEC88602FC7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "The nucleotide sequence of the mercuric resistance operons of plasmid R100 and transposon Tn501: further evidence for mer genes which enhance the activity of the mercuric ion detoxification system."; Mol. Gen. Genet. 202:143-151(1986).
                                                                                                               Shigella flexneri.
Plasmid virulence plasmid pWR501.
Bacteria; Proteobacteria; gamma subdivision;
                                                                                                                                                                                             Q9AFK4;
01-JUN-2001 (TrEMBLrel. 17,
01-JUN-2001 (TrEMBLrel. 17,
01-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE-96105204; PubMed-8529897;
Reniero D., Galli E., Barbieri P.;
"Cloning and comparison of mercury- and organomercurial-resistance determinants from a Pseudomonas stutzeri plasmid.";
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J. Mol. Biol. 230:1103-1107(1993).
                                                                                                                                                                   MERR.
                                                                                                                                                                               In501 repressor.
                                                                                                                                                                                                                                                             Q9AFK4
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EMBL; U90263; AAC38229.1; -.
InterPro; IPR000551; HTH_MerR.
Pfam; PF00376; merR; 1.
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Kholodii G.Ya, Yurieva O.V., Lomovskaya O.L.,
Mindlin S.Z., Nikiforov V.G.;
                                           SEQUENCE FROM N.A. MEDLINE=21189246; PubMed=11292750;
                                                                                                      Shigella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-98148002; PubMed-9479042; Renlero D., Mozzon E., Galli E., Barbieri P.; Mozzon E., Galli E., Barbieri P.; Two aberrant mercury resistance transposons in the Pseudomonas stutzeri plasmid pPB.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SPECIES=P.stutzeri; STRAIN=OX; PLASMID=PPB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=86174347; PubMed=3007931; Brown N.L., Misra T.K., Winnie J.N., Schmidt
               Venkatesan M.M., Goldberg M.B.,
Blattner F.R.;
                                                                                        NCBI_TaxID=623;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gene
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 Complete DNA sequence and analysis of the
                                                                                                                                                                                                                                                                                                                                      79
                                                                                                                                                                                                                                                                                                                                                                  59 GTHCEEASSLAEHKLKDVREKMADLARME 87
                                                                                                                                                                                                                                                                                                                                                                                                            Local
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SIMILARITY: BELONGS TO THE MERR
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                                                                                                                                                                                                                                                                                                                                      GTHCEEASSLAEHKLKDVREKMADLARME 107
                                                                                                                                                                                                                                                                                                                                                                                               . Similarity
29; Conser
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                                                                                                                                                                                                                                                                                                                                                                                           24.8%; Solitarity 100.0%; I conservative 0;
                                                                                                                                                                                                                                                           PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                            b; Score 29; DB
b; Pred. No. 7.9
0; Mismatches
                                                                                                                                                                                            Created)
Last sequence update)
Last annotation update)
                             Rose D.J., Grotbeck E.J.,
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                                                                                                                                                                                                                                                             172
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7.9e-1
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                                                                                                                                                                                                                                                                                                                                                                                                            .9e-23;
large virulence plasmid of
                                                                                                                       Enterobacteriaceae;
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RESULT 8
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Best Local :
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Q57492;
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SMART; SM00422; HTH_MERR; 1.

PROSITE; PS00552; HTH_MERR_FAMILY; 1.

DNA-binding; Plasmid; Transcription regulation.

DNA-binding; Plasmid; Transcription regulation.

SEQUENCE 172 AA; 18826 MW; 897D139E7BC182A9 CRC64;
                                                                                                                                                                                               PRINTS; PR00040; HTHMERR.
SMART; SM00422; HTH_MERR; 1.
PROSITE; PS00552; HTH_MERR_FAMILY; 1.
DNA-binding; Transcription regulation.
SEQUENCE 151 AA; 16559 MW; 238460FCE51754AD CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-NOV-1996 (TREMBLIEL 01, 01-NOV-1996 (TREMBLIEL 01, 01-JUN-2001 (TREMBLIEL 17,
                                                                                                                                                                                                                                                            EMBL; Z33486; CAA83894.1; -.
EMBL; Z33485; CAA83893.1; -.
EMBL; Z33485; CAA83893.1; -.
InterPro; IPRO00551; HTH_MerR.
Pfam; PF00376; merR; 1.
                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-SO1;
Osborn A.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Klebsiella oxytoca.
Bacteria; Proteobacteria;
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Pfam; PF00376; nerR; 1
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                                                                                                                                                                                                                                                                                                                        Submitted (MAY-1994) to -!- SIMILARITY: BELONGS
                                                                                                                                                                                                                                                                                                                                                Osborn A.M.;
                                                                                                                                                                                                                                                                                                                                                                                                Submitted (DEC-1994) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Enterobacter
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Regulatory protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Infect. Immun. 69:3271-3285(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Shigella flexneri."
                                                                                                                                                                                                                                                                                                                                                              STRAIN-SE31;
                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=550, 571;
                                                                                                  109
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                                                                                                                         31 VLSELVCACHARKGNVSCPLIASIQ 55
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                                                                                                  VLSELVCACHARKGNVSCPLIASLQ 133
                                                                                                                                                  l Similarity
25; Conserv
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29; Conserv
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ilarity 100.0%;
Conservative (
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TO THE MERR FAMILY OF
                                                                                                                                                                                                                                                                                                                                                                                                            Strike P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gamma subdivision; Enterobacteriaceae;
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                                                                                                                                                                        Score 25;
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9.3e-23;
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01-JUL-1997 01-NOV-1999

(TrEMBLrel. 04, (TrEMBLrel. 12,

Last sequence update)

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Matches 25
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Q57106; O08282; O08130; O08287; O08166; O08288; O08185;
Q1-NOV-1996 (TrEMBLrel. 01, Created)
Q1-NOV-1996 (TrEMBLrel. 01, Last sequence update)
Q1-DEC-2001 (TrEMBLrel. 19, Last annotation update)
Regulatory protein (Mercury resistance operon regulatory protein) (MER operon regulatory protein).
Submitted (DEC-1994) to t [2]
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SMART; SM00422; HTH_MERR; 1.
PROSITE; PS00552; HTH_MERR_FAMILY; 1.
DNA-binding; Transcription regulation.
DNA-binding; Transcription 17CC8F1005A33FD0 CRC64;
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MERR protein (Mercuric resistance operon regulatory protein).
                                                                                                                                                                                                                                                                                                                                             Acinetobacter sp., and Acinetobacter sp. LS56-7.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                               Acinetobacter.
                                                                                                                                                                                                                                                                                                              Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                            Enterobacter cloacae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Alcaligenes sp.,
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Racteria; Proteobacteria
                                                                                                                 STRAIN-SE12;
                                                                                                                                                             SEQUENCE FROM
                                                                                                                                                                                                                                   NCBI_TaxID=471, 562, 512,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pantoea agglomerans,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Escherichia coli,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Acinetobacter calcoaceticus,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Molecular genetic analysis of the Tn5041 transposition system."; \alpha (uss. J. Genet. 36:365-373(2000).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          likiforov V.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  25;
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                               , Strike P., Ritchie D.A.;
the EMBL/GenBank/DDBJ databases.
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b; Pred. No. 1.5
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                                                                                                                                                                                                                                       472, 107402;
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Best Local S
Matches 25
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EMBL; X08993; CAA70195.1; -.
EMBL; Z33483; CAA83891.1; -.
EMBL; Z33482; CAA83890.1; -.
EMBL; X08992; CAA70185.1; -.
EMBL; Y08992; CAA70237.1; -.
EMBL; A7245842; CAC80722.1; -.
EMBL; A7245866; CAC38823.1; -.
EMBL; A7250860; CAC38823.1; -.
                                                                                                                                                                                                                                                                                                                                                                                           01-MAY-2000 (TREMBLIGEL 13, 01-MAY-2000 (TREMBLIGEL 13, 01-JUN-2001 (TREMBLIGEL 17,
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SMART; SM00422; HTH_MERR; 1.

PROSITE; PS00552; HTH_MERR_FAMILY; 1.

DNA-binding; Plasmid; Transcription regulation.

DNA-binding; Plasmid; Transcription regulation.

SEQUENCE 151 AA; 16529 MW; 239350FCE51754AD CRC64;
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STRAIN-CH210; TRANSPOSON-TN5059;
MEDLINE-97303088; PubMed-9159519;
Yurieva O., Kholodii G., Minakhin L.,
Mindlin S., Nikiforov V.;
"mer sequences on plasmids." submitted (SEP-1998) to the EMBL; AF092070; AAD52706.1;
                                                                              SEQUENCE FROM N.A.
STRAIN=KT2440;
Bruce K.D., Lilley A.K.,
                                                                                                                                                                                                                                                   Pseudomonas putida.
Plasmid group 5 plasmid.
Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. SPECIES-Acinetobacter sp. LS56-7; PLASMID-PKLH204;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "pKLH2-like aberrant transposons and possible mechanisms dissemination.";
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                                                                                                                                                                                                                                                                                                                                                                    MerR (Fragment).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9R9W9;
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                                                                                                                                                                                               NCBI_TaxID=303;
                                                                                                                                                                                                                              Pseudomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Kholodii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=21272500; PubMed=11376944;
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Gene 269:121-130(2001).
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                                                                     Bailey M.J.;
                                                                                                                                                                                                                                                      gamma
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                            EMBL/GenBank/DDBJ
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Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
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Q60233; P75015; Q44314; Q51768; Q51808; Q52601; Q56390; Q56443;
O1-NOV-1996 (TrembLrel. 01, Created)
O1-NOV-1996 (TrembLrel. 01, Last sequence update)
O1-MAR-2002 (TrembLrel. 20, Last annotation update)
Mercuric resistance operon regulatory protein (MERR protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              xanthomonas, and
Pseudomonas sp. (strain ADP).
Plasmid pMER327, Plasmid RP1, and Plasmid pADP-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Comamonas testosteroni
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Alcaligenes sp.,
Pseudomonas fluorescens,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                       "The sequence of the mer operon of pMER327/419 and transposon ends pMER327/419, 330 and 05."; Gene 146:73-78(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SPECIES-Alcaligenes sp., and P.fluorescens; TRANSPOSON-TN5053; MEDLINE-94341572; PubMed-8063107; Hobman J., Kholodii G., Nikiforov V., Ritchie D.A., Strike P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            unidentified,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       InterPro;
                                                                                                                                                                                                   "Four genes, two ends, and a res region are involved in transposition of Tp5053: a paradigm for a novel family of transposons carrying either a mer operon or an integran."; Mol. Microbiol. 17:1189-1200(1995).
                                                                                                                                                                                                                                                                                                                                                  Osborn A.M., Bruce K.D., Strike P., Ritchie D.A.; Submitted (DEC-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                          SPECIES=C.testosteroni; STRAIN=SE3;
                                                                    SPECIES=Xanthomonas; PLASMID=RPI; TRANSPOSON=TN5053; MEDLINE=93253772; PubMed=8387603;
                                                                                                                                                           SPECIES=unidentified;
                                                                                                                                                                                                                                                             Nikiforov V.G.;
                                                                                                                                                                                                                                                                          MEDLINE=96130850; PubMed=8594337;
Kholodii G.Y., Mindlin S.Z., Bass I.A.,
                                                                                                                                                                                                                                                                                                         SPECIES=unidentified;
                                                                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NCBI_TaxID=512, 294, 285, 32644, 338, 47660;
             Kholodii G.Ya., Yurieva O.V., Lomovskaya O.L., Gorlenko Zh.M., Mindlin S.Z., Nikiforov V.G.; "Tn5053, a mercury resistance transposon with integron's ends."; J. Mol. Biol. 230:1103-1107(1993).
                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                               Kholodii
                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Kurieva O.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Similarity
                                                                                                                                Genet. 31:1447-1451(1995).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 2; Lo
                                                                                                                                                                                                                                                                            Yurieva O.V., Minakhina S.V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0,
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RESULT 12
Q934S8
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                                                  Matches
                                                                           Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SPECIES-PSeudomonas sp. (strain ADP); STRAIN-ADP; PLASMID-PADB
MARTINEZ B.M., Tomkins J., Wackett L.P., Wing R., Sadowsky M.:
Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY; BELONGS TO THE MERR FAMILY OF TRANSCRIPTIONAL
                                                                                                                                                                                                                                                                                                                                                                             Q934S8 PRELIMINARY; PRT; 151 AA.

Q934SB;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRINTS; PR00040; HTHMERR.
SMART; SM00422; HTH_MERR; 1.
PROSITE; PS00552; HTH_MERR_FAMILY; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR000551; HTH_MerR.
Pfam; PF00376; merR; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Activator; DNA-binding; Mercuric resistance; Mercury; Plasmid;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           -!- SIMILARITY: BELONGS
                                                                                                  PROSITE; PS00552; HTH_MERR_FAMILY; UNKNOWN_1.
DNA-binding; Transcription regulation.
SEQUENCE 151 AA; 16555 MW; 26DDF7A510B082
                                                                                                                                                                                                                                              Kalyaeva E.S., Kholodii G.Y., Bass I.A., Gorlenko A.M., Yurieva O.V.,
Nikiforov V.G.;
                                                                                                                                                                                                                                                                                                                             Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                         Thiobacillus ferrooxidans
                                                                                                                                                                                                                                                                                                                                                                  Mer operon regulatory protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Repressor;
                                                                                                                                                                                                                                                                          STRAIN=G66;
                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                               NCBI_TaxID=920;
                                                                                                                                          Pfam; PF00376; merR; 1.
                                                                                                                                                                    EMBL; AJ251743; CAC69248.1; -.
                                                                                                                                                                                              russ. J. Genet. 37:972-975(2001).
-i- SIMILARITY: BELONGS TO THE MERR FAMILY OF TRANSCRIPTIONAL
                                                                                                                                                                                                                     ferrooxidans.";
                                                                                                                                                                                                                                   "Tn5037, a Tn21-like mercury resistance transposon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                113 LYCACHARKGNVSCPLIASLQG 134
                                                                                                                                                      InterPro; IPR000551; HTH_MerR.
 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            35 LVCACHARKGNVSCPLIASLQG 56
                        35 LYCACHARKGNVSCPLIASLQ 55
                                                                Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REGULATORS.
                                                                                                                                                                               REGULATORS
Similarity
                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Transcription regulation. 144 AA; 16060 MW; E4B3E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                         TRANSPOSON=TN5037;
                                                    Conservative
                                                                                                                                                                                                           37:972-975(2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18.8%; 50
100.0%; Pr
                                                              17.9%; Score 21; DB 2; 100.0%; Pred. No. 2.6e-1
                                                                                                                                                                                                                                                                                                                             gamma subdivision; Acidithiobacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 22;
Pred. No.
                                                     0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     E4B3EFEECA317F2D CRC64;
                                                                                                     26DDF7A510B0829B CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mismatches
                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2.1e-15;
                                                              2.6e-14;
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                                                                              Length 151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
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                                                                                                                                                                                                                                       from Thiobacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0;
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Q44191 ID C

044191

PRELIMINARY;

PRT;

151

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RESULT 13

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RESULT 14
099093
1D 09909
AC 09909
AC 09909
DT 01-NO
DT 0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Q99093; PRELIMINARY; PRT; 151 AA. Q99093; O1-NOV-1996 (TrEMBLrel. 01, Created) O1-NOV-1996 (TrEMBLrel. 01, Last sequence update) O1-MAR-2002 (TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SPECIES-A.calcoaceticus; PLASMID-PKLH2; Lomovskaya O.L., Nikiforov V.G.; Genetika 24:1064-1071(1988).
                       SPECIES=A.lwoffii; PLASMID=PKLH103, PKLH102, AND PKLH104; Kholodii G.Y., Mindlin S.Z., Lomovskaya O.L., Gorlenko Z.
                                                                                                                                                                                                                                                                                                                                                             SPECIES=A.calcoaceticus; PLASMID=PKLH2; MEDLINE=94134837; PubMed=8302940;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Acinetobacter sp.
Plasmid pKLH2, Plasmid pKLH103, Plasmid pKLH102, Plasmid pKLH104,
                                                                                                                                                                                Plasmid 30:303-308(1993).
                                                                                                                                                                                                                   "Molecular characterization of an aberrant mercury resistance transposable element from an environmental Acinetobacter stra
                                                                                                                                                                                                                                                                                        Kholodii G.Y., Lomovskaya O.L., Gorlenko Z.M., Mindlin Yurieva O.V., Nikiforov V.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Plasmid pKLH205
                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID-471,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Acinetobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Acinetobacter
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Acinetobacter calcoaceticus,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MERR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mer operon regulatory protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRINTS; PRO0040; HTHMERR.
SMART; SM00422; HTH_MERR; 1.
PROSITE; PS00552; HTH_MERR_FAMILY; 1.
DNA-binding; Transcription regulation.
DNA-binding; Transcription $$848460FCE50240FC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Osborn A.M., Bruce K.D., Strike P., Ritchie D.A.; "Sequence Conservation between Regulatory Mercury Resistance Genes from Mercury Polluted and Pristine Environments."; Submitted (MAY-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-NOV-1996 (TrEMBLrel.
01-NOV-1996 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Q44191;
01-NOV-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Regulatory protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRAIN-T2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=358;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Agrobacterium tumefaciens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    REGULATORS.; Z33487; CAA83895.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LAEHKLKDVREKMADLARME
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20;
0.V.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Proteobacteria; gamma subdivision; Moraxellaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
Nikiforov V.G.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              lwoffii,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              28090, 472;
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100.0%; Pr
.-- 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01, Created)
01, Last sequence update)
19, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              107
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         THE MERR FAMILY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 20;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL/GenBank/DDBJ databases.
THE MERR FAMILY OF TRANSCRIPTIONAL
                                                                                                                                                                                                           environmental Acinetobacter strain.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       .9e-13;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                       Z.M.,
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RESULT 15
Q935L5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Best
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q935L5 PRELIMINARY;
Q935L5;
O1-DEC-2001 (TIEMBLEEL 19, C:
01-DEC-2001 (TIEMBLEEL 19, L:
01-MAR-2002 (TIEMBLEEL 20, L:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AF213017; AAA19678.1; -.
EMBL; AJ251539; CAB65953.1; -.
EMBL; AJ251517; CAB65939.1; -.
EMBL; AJ251009; CAB65945.1; -.
EMBL; AJ251009; CAB65949.1; -.
EMBL; AJ251706; CAC39408.1; -.
EMBL; AJ251706; CAC39408.1; -.
InterPro; IPRO00551; HTH_MerR.
Pfan; PP00376; merR; 1.
Pfam; PF00376; merR; 1.
PROSITE; PS00552; HTH_MERR_FAMILY; UNKNOWN_1.
DNA-binding; Plasmid; Transcription regulation;
SEQUENCE 151 AA; 16589 MW; 239344ADA01754AD
                                                                                                                                                                                                         Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihla M. Baker S., Basham D., Brooks K., Chillingworth T., Connerton P., Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J., Feltwell T., Hamlin N., Haque A., Hien T.T., Holroyd S., Jagels K., Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,
                                                                                   EMBL; AL513383; CAD09746.1;
                                                                                                                                    Nature 413:848-852(2001)
                                                                                                                                                 "Complete genome sequence of a enterica serovar Typhi CT18.";
                                                                                                                                                                                               Quail M., Rutherford K., Simmonds M., Skelton
                                                                                                                                                                                                                                                                                                                               STRAIN-CT18
                                                                   InterPro; IPR000551; HTH_MerR.
                                                                                                                                                                                    Whitehead
                                                                                                                                                                                                                                                                                                          MEDLINE=21534947; PubMed=11677608;
                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                          Salmonella
                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                      Plasmid pHCM1
                                                                                                                                                                                                                                                                                                                                                                                                                                      Salmonella typhi.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Putative mercuric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRINTS; PRO0040; HTHMERR.
SMART; SM00422; HTH_MERR; 1.
PROSITE; PS00552; HTH_MERR_FAMILY; 1.
DNA-binding; Plasmid; Transcription regulation.
DNA-binding; Plasmid; Ts49350FCE50240FC CRC64;
                                                                                                                  1 SIMILARITY: BELONGS TO THE MERR FAMILY OF
                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=601;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "The shuffling function of resolvases."; Gene 269:121-130(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SPECIES=Acinetobacter sp.; STRAIN=ED45-25; PLASMID=PKLH205; MEDLINE=21272500; PubMed=11376944;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "pKLH1-like aberrant mercury resistance transposons of environmental Acinetobacter strains: spread, polymorphism and possible origin."; Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           10 LAEHKLKDVREKMADLARME 29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                               S., Barrell B.G.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                     resistance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  100.08;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Last sequence update)
Last annotation update)
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Pred. No.
                                                                                                                                                             multiple drug resistant Salmonella
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. 2.9e-13;
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                                                                                                                                                                                            J., Stevens K.,
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        CRC64;
                  Complete proteome.
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Query Match 17.1%; Score 20; DB 16; Length 151; Best Local Similarity 100.0%; Pred. No. 2.9e-13; Matches 20; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Search completed: May 28, 2003, 10:41:38 Job time: 85 secs

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Maximum DB seq length: 200000000
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score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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1: /cgn2-6/ptodata/1/
2: /cgn2-6/ptodata/1/
3: /cgn2-6/ptodata/1/
4: /cgn2-6/ptodata/1/
6: /cgn2-6/ptodata/1/
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/cgn2_6/ptodata/1/laa/5B_COMB.pep:*
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  В
US-09-100-414B-105
US-09-303-323-105
5198345-12
US-09-303-323-106
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US-09-303-323-106
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US-09-172-952-16
US-09-174-141A-69
US-09-174-141A-69
US-09-174-634D-19
US-08-403-866-2
US-08-960-022-8
US-08-965-310A-5
US-08-965-310A-5
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US-09-382-950-7
US-09-382-736B-8
US-09-619-103-9
US-09-619-103-9
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                                                                                                                                                                                          Sequence 2, Appli
Sequence 7, Appli
Sequence 8, Appli
Sequence 9, Appli
Sequence 105, App
Sequence 105, App
Patent No. 5198345
Sequence 106, App
Sequence 106, App
Sequence 4258, App
                                                                                                                                                                                                                                                                                                                    Description
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Sequence 4, Appli
Sequence 4, Appli
Sequence 4, Appli
Sequence 18, Appli
Sequence 18, Appl
Sequence 14, Appl
Sequence 28, Appl
Sequence 28, Appl
Sequence 69, Appl
Sequence 69, Appl
                           Sequence 19, Appli
Sequence 2, Appli
Sequence 8, Appli
Sequence 2, Appli
Sequence 2, Appli
     Sequence
               Sequence
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RESULT 2 US-09-382-950- Sequence 7, Patent No. 6 GENERAL INFO APPLICANT: APPLICANT: APPLICANT: APPLICANT: CURRENT AFF CURRENT	Query Matc Best Local Matches Qy 110 WS Db 1 WS	RESULT 1 US-08-948-097- Sequence 2, Patent No. 6 Patent No. 6 PATENT NO. 6 PAPLICANT: APPLICANT: TITLE OF IN FILE REFERSE CURRENT FIL EARLIER APP CURRENT FIL EARLIER FIL HUMBER OF S SEQ ID NO 2 LENGTH: B TYPE: PRT ORGANISM: FEARURE: NAME/KEY: NAM	44440 544 544 544 544 544 544 544 544 54
950-7 7, Application US/09382950 80, 6303337 NAT: Rothschild, Kenneth ANT: Gite, Sadanand ANT: Olejnik, Jerzy Derminal and C-Terminal Markers PRILICATION: N-Terminal and C-Terminal Markers OF INVENTION: N-Terminal and C-Terminal Markers OF INVENTION: NUMBER: US/09/382,950 T APPLICATION NUMBER: US/09/382,950 T FILING DATE: 1999-08-25 OF SEQ ID NOS: 17 RE: Patentin version 3.0 NO 7 H: 8 PRT ISM: Artificial/Unknown	atch 6.8%; Score 8; DB 7, Deny 100 08; Pred. No. 2e+05; cal 8; Conservative 0; Mismatches 0; Inde WSHPQFEK 117	Application US/08948097C 103493 103493 Sketra, Arne Voss, Selma VCSS, Selma VCSTION: Streptavidin Muteins NCE: HUBR 1119 LICATION NUMBER: US/08/948,097C LICATION NUMBER: DE 196 41 876.3 LING DATE: 1997-10-10 SEQ ID NOS: 17 SEQ ID NOS: 17 SEQ ID NOS: 17 BINDING B	5.1 640 4 US-09-362-871-2 Se 6 5.1 983 2 US-08-164-2928-26 Se 6 5.1 983 3 US-08-845-623-26 Se 6 5.1 983 3 US-08-815-927-26 Se 6 5.1 983 4 US-09-435-242-26 Se 6 5.1 1004 4 US-09-9435-242-26 Se 6 5.1 1162 4 US-09-9435-242-26 Se 6 5.1 2547 3 US-09-058-489-35 Se 6 5.1 2547 3 US-09-058-489-36 Se 6 5.1 2547 3 US-09-958-489-36 Se 6 5.1 2547 3 US-09-918-148-22 Se 6 5.1 2547 3 US-09-918-148-25 Se 6 4.3 9 4 US-09-382-9368-10 Se 6 4.3 13 4 US-09-817-913-25 Se 6 4.3 13 4 US-09-917-913-25 Se 6 4.3 13 4 US-09-917-913-25 Se 6 4.3 13 4 US-09-917-913-25 Se 6 4.3 13 4 US-09-017-918-11 Se 6 4.3 13 4 US-09-100-4148-11 Se
in Nascent Proteins	ls 0; Gaps 0;		Sequence 2, Appli Sequence 26, Appl Sequence 26, Appl Sequence 26, Appl Sequence 26, Appl Sequence 27, Appli Sequence 27, Appli Sequence 35, Appli Sequence 36, Appli Sequence 27, Appli

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Query Match
Best Local Similarity
""" hes 8; Conserve
                                                                               ; OTHER INFORMATION: designed sequence to act as an identifying tag US-09-619-103-9
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US-09-619-103-9
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                                                                                                                                                                                       SEQ ID NO 9
                                                                                                                                                                                                                                                                                                                                                                     Sequence 9, Application US/09619103
Patent No. 6429300
GENERAL INFORMATION:
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; NAME/KEY: misc_feature
; LOCATION: ()..()
; OTHER INFORMATION: Synthetic
US-09-382-950-7
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                                                                                                                                                                                                              APPLICANT: Kurz, Markus
APPLICANT: Lohse, Peter
APPLICANT: Lohse, Peter
APPLICANT: Wagner, Richard
TITLE OF INVENTION: Peptide Acceptor Ligation Methods
FILE REFERENCE: 50036/031002
CURRENT APPLICATION NUMBER: US/09/619,103
CURRENT FILING DATE: 2000-07-19
PRIOR APPLICATION NUMBER: 05/145,834
NUMBER OF SEQ ID NOS: 26
SOPTMARER: Estatos
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQ ID NO 8
LENGTH: 8
TYPE: PRT
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                                                                                                                        TYPE: PRT
ORGANISM: Artificial Sequence
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Patent No. 6306628
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Rothschild, Kenneth
APPLICANT: Gite, Sadanand
APPLICANT: Gite, Sadanand
APPLICANT: Olejnik, Jerzy
TITLE OF INVENTION: Methods for the Detection, Analysis and Isolation of Nascent Prot
FILE REFERENCE: AMBER-03951
CURRENT APPLICATION NUMBER: US/09/382,736B
CURRENT FILING DATE: 1999-08-25
NUMBER OF SEQ ID NOS: 18
SOFTWARE: PatentIn version 3.0
                                                                                                                                                                         LENGTH:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  110 WSHPQFEK 117
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Local Similarity 100.0%; Pred. No. 2e-
les 8; Conservative 0; Mismatches
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                         Conservative
                100.08; F1
                                 6.8%; Score 8;
100.0%; Pred. No.
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                      Mismatches
                                             DB 4; Length 8;
2e+05; Indels
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Thes 0; Indels
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           0; Gaps
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           0,
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Sequence 105, Application US/09303323
Patent No. 6228987
GENERAL INFORMATION:
APPLICANT: Wang, Chang Yi
TITLE OF INVENTION: NOVEL LHRH PEPTIDE
TITLE OF INVENTION: IMMUNOGENS
NUMBER OF SEQUENCES: 106
                                                                                                                                                                                                                                                      US-09-303-323-105
                                                                                                                                                                                                                                                                        RESULT 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                      TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: peptide
US-09-100-414B-105
                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity 100.0%; Pred. No. 11.
Matches 6; Conservative 0; Mismatches
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ZIP: 10134 VV...
COMPUTER READABLE FORM:
TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: 212-751-6849
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 105, Application US/09100414B Fatent No. 6025468
GENERAL INFORMATION:
                                                                                                                                 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-758-4800
TELEFAX: 212-751-6849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/0:
FILING DATE: 20-JUNE-1990
CLASSIFICATION: 424
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                          COUNTRY:
                                                                           STATE:
                                                                                     CITY: New York
                                                                                                       STREET:
                                                                                                                  ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morgan & Finnegan, L.L.P.
                                                                                                                                                                                                                                                                                                                  13 RMETVL 18
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TITLE OF INVENTION: NOVEL
TITLE OF INVENTION: IMMUNI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Maria H. Lin
REGISTRATION NUMBER: 29,323
REFERENCE/DOCKET NUMBER: 11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: MOLY...
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                                                           USA
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                                                                                                    Morgan & Finnegan, L.L.P.
5 Park Avenue
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o. 11;
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0;

SOFTWARE: Word 97
CURRENT APPLICATION DATA:

OPERATING SYSTEM:

IBM PC compatible SYSTEM: PC Windows

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US-09-100-414B-106
; Sequence 106, Application US/09100414B
; Patent No. 6025488
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5198345-12
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5198345-12
; Patent No. 5198345
                                                                                                                                                                                                                                                                           RESULT 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/
FILING DATE: 20-DEC-1985
SEQ ID NO:12:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: GWYNNE, DAVID I.; BUXTON, FRANCIS P.; PICKETT, MARK H.; DAVIES, ROGER W.; SCAZZOCCHIO, CLAUDIO
TITLE OF INVENTION: VECTORS IN USE IN FILAMENTOUS FUNGI
NUMBER OF SEQUENCES: 28
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
Matches 6; Conserv
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                                                                                                                                                                                                 GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO: 105:
                                                                                   NUMBER OF SEQUENCES: 106
CORRESPONDENCE ADDRESS:
ADDRESSEE: Morgan & Finnegan, L.L.P.
                                                                                                                                     APPLICANT: Wang, Chang Yi
TITLE OF INVENTION: NOVEL LHRH PEPTIDE
TITLE OF INVENTION: IMMUNOGENS
                 STREET: 3%
CITY: New York
CTATE: NY
TATE: NY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REGISTRATION NUMBER: 29,323
REFERENCE/DOCKET NUMBER: 11.
TELECOMUNICATION INFORMATION:
TELEPHONE: 212-758-4800
TELEFAX: 212-751-6849
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 19 amino acids
TYPE: amino acid
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ATTORNEY/AGENT INFORMATION:
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ZIP: 10154-0054
                                                 ADDRESSEE: Molyu...
ADDRESSEE: Molyu...
ADDRESSEE: Molyu...
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                                                                                                                                                                                                                                                                                                                                 9 LSELVC 14
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                                                                                                                                                                                                                                                                                                                                                                                             5.1%; Score 6; DB lilarity 100.0%; Pred. No. 14 Conservative 0; Mismatches
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RESULT 9
US-09-303-323-106
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Patent No. 6228987
GENERAL INFORMATION:
APPLICANT: Wang, Chang X1
TITLE OF INVENTION: MOVEL LHRH PEPTIDE
TITLE OF INVENTION: IMMUNOGENS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 106, Application US/09303323 Patent No. 6228987
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Matches 6; Conserv
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                                                 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: 11
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-758-4800
TELEFAX: 212-751-6849
INFORMATION FOR SEQ ID NO: 106:
                                                                                                   TELEPHONE: 212-758-4800
                                                                                                                                    ATTORNEY/AGENT INFORMATION:
NAME: MAILA H. Lin
REGISTRATION NUMBER: 29,323
REFERENCE/DOCKET NUMBER: 11:
                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE: 20-JUNE
                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                         SOFTWARE: Word 97
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 1
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC Windows
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
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ATTORNEY/AGENT INFORMATION:
NAME: Maria H. Lin
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                                                                   TELEPHONE: 212-751-6849
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OPERATING SYSTEM:
                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/0:
FILING DATE: 30-APR-1999
                                                                                                                                                                                                                                                         CLASSIFICATION:
TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: New York
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SOFTWARE: Word 97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Morgan & Finnegan, L.L.P. STREET: 345 Park Avenue
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                                ENGTH:
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                 amino acid
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IBM PC compatible
SYSTEM: PC Windows
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100.0%; Pred. No. 17;
1tive 0; Mismatches
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APPLICATION NUMBER:

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; MOLECULE TYPE: peptide US-09-303-323-106
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LENGTH: 61
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CURRENT APPLICATION NUMBER: US/09/134,001C
CURRENT FILING DATE: 1998-08-13
PRIOR APPLICATION NUMBER: US 60/064,964
PRIOR FILING DATE: 1997-11-08
PRIOR APPLICATION NUMBER: US 60/055,779
PRIOR PILING DATE: 1997-08-14
                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
APPLICANT: Van den BOOGAART, Paul
APPLICANT: KOK, Jacobus Johannus
APPLICANT: VERMEULEN, Arnoldus Nicolaas
TITLE OF INVENTION: COCCIDIOSIS POULTRY VACCINE
NUMBER OF SEQUENCES: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Lynn Doucette-Stamm et al TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO STAPHYLOCOCCUS TITLE OF INVENTION: EPIDERMIDIS FOR DIAGNOSTICS AND THERAPEUTICS
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                                                                                                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
FILING DATE: 06-JUN-19
                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS: Akzo No. 5670362el Patent Department
                                                         CLASSIFICATION: 435
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
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Local Similarity . 100.0%; Pred. No.
les 6; Conservative 0; Mismatch
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                                                                                                                                                          COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                APPLICATION NUMBER: US 08/310,357 FILING DATE: 21-SEP-1994
                                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                     STATE: Maryland
                                                                                                                                                                                                                                                                                                                             CITY: Rockville
                                                                                                                                                                                                                                                                                                                                              STREET:
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les 6; Conserv
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100.0%; Pred. No. 32;
tive 0; Mismatches
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US-08-468-855-4
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                                                 PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/604,075
FILING DATE: 18-JUN-1992
PRIOR APPLICATION NUMBER: EP 91,201.523.7
FILING DATE: 18-Jun-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION:
TELEPHONE: (301) 258-5200
INFORMATION FOR SEQ ID NO: 4:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: EP 91
FILING DATE: 18-Jun-1991
ATTORNEY/AGENT INFORMATION:
NAME: MATY E. GOTTLEY
REGISTRATION NUMBER: 34,4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 135 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: FILING DATE: 18-JUN-PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATE: Patentin Release #1.0, Version #1.25
SOFTWARE: Patentin NDATA:
APPLICATION DATA:
APPLICATION NUMBER: US/08/468,855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: van den BOOGAART, Paul
APPLICANT: KOK, Jacobus Johannus
APPLICANT: VERMEULEN, Arnoldus Nicolaas
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                                                                                                                                                                                                   CLASSIFICATION: 435
PRIOR APPLICATION UMBER: US 08/310,357
FILING DATE: 21-SEP-1994
PRIOR APPLICATION UMBER: US 08/102,865
APPLICATION NUMBER: US 08/102,865
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: Akzo No. 5780289el Patent Department
STREET: 1300 Piccard Drive
                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: COCCIDIOSIS POULTRY VACCINE NUMBER OF SEQUENCES: 10
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NAME: Mary E. Gormley REGISTRATION NUMBER: 34 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                      FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Rockville
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06-AUG-1993
                                                                                                                                                                                        06-AUG-1993
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                                                                                                                                                                                                                                                                                                                                                                                                                              Floppy disk
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100.0%; Pr
170 0;
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RESULT 13
US-08-310-357-4
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Matches
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                                                                                                                                                                                                                                    TELEPHONE: (301) 258-
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: van den BOOGAART, Paul
APPLICANT: KOK, Jacobus Johannus
APPLICANT: VERMEULEN, Arnoldus Nicolaas
TITLE OF INVENTION: COCCIDIOSIS POULTRY VACCINE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
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LENGTH: 135 amino acid
                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                       FILING DATE: 18-Jun-1991
ATTORNEY/AGENT INFORMATION:
NAME: William M. Blackstone
REGISTRATION NUMBER: 29,772
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                    MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
ZIP: 208
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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CITY: Rockville
STATE: Maryland
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nes 6; Conserv
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 41
                                                                 Local Similarity
les 6; Conserv
                                                                                                                                                                  TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER:
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 EEASSL 46
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                                                                 Conservative
                                                                                                                                                                  linear
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                                                               5.1%; Score 6; DB : 100.0%; Pred. No. 65 tive 0; Mismatches
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US-08-468-852-4
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US-08-468-857-4
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Patent No. 5792644
                                                                                                                                          Sequence 4, Application US/08468857 Patent No. 5925347
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                 GENERAL INFORMATION:
APPLICANT: Van den BOOGAART, Paul
APPLICANT: KOK, Jacobus Johannus
APPLICANT: VERWEULEN, Arnoldus Nicolaas
TITLE OF INVENTION: COCCIDIOSIS POULTRY VACCINE
NUMBER OF SEQUENCES: 10
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: van den BOOGAART, Paul APPLICANT: KOK, Jacobus Johannus APPLICANT: VERMEULEN, Arnoldus Nicolaas TITLE OF INVENTION: COCCIDIOSIS POULTRY VACCINE NUMBER OF SEQUENCES: 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US 07/604,075
FILING DATE: 18-JUN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 91.201.523.7
FILING DATE: 18-JUN-1991
ATTORNEY/AGENT INFORMATION:
NAME: MAIY E. GOTMLEY
PROTECTION NUMBER: AND TO THE PROPERTY NAME: MAIY E. GOTMLEY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: amino acids
TYPOLOGY: 115-4
YOLECTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 0 FILING DATE: 06-AUG-1993 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/310,357
FILING DATE: 21-SEP-1994
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ZIP: 20850
COMPUTER READABLE FORM:
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/01
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                            y Match 5.1%; Score 6; DB:
Local Similarity 100.0%; Pred. No. 65
hes 6; Conservative 0; Mismatches
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                                                                                                                                                                                                                                                                                                                    5 EEASSL 10
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ADDRESSEE: Akzo No. 592347el Patent Department
CITY: Rockville
STATE: Maryland
COUNTRY: MOSTANA
IP: 20850 0.5.A.
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Total number of hits satisfying chosen parameters:
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DB seq length: 2000000000
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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09 10 100 310 309	TE-10-103-313-350	US-10-026-578B-11	US-10-026-578B-10	US-09-809-517A-34	US-09-809-517A-31	US-10-026-578B-4	US-10-026-578B-3	US-09-809-517A-33	US-09-809-517A-30	US-09-983-067-3	US-09-973-145-7	US-09-809-517A-9	US-10-174-368A-7	US-10-026-578B-9	US-10-026-578B-2	US-10-001-934-8	US-10-208-357-9	US-10-104-218-5	US-09-809-517A-6	ID
sequence 333, App		11,	Sequence 10, Appl	Sequence 34, Appl	Sequence 31, Appl	Sequence 4, Appli	Sequence 3, Appli	Sequence 33, Appl	Sequence 30, Appl	Sequence 3, Appli	Sequence 7, Appli	Sequence 9, Appli	Sequence 7, Appli	Sequence 9, Appli	Sequence 2, Appli	Sequence 8, Appli	Sequence 9, Appli	Sequence 5, Appli	Sequence 6, Appli	Description

45	44	43	42	41	40	39	38	37	36	35 5	34	ω ω	32	31	30	29	28	27	26	25	24	23	22	21	20
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US-09-764-868-992	US-09-925-300-1191	US-09-557-796-28	US-09-557-796-16	US-10-140-293-37	US-10-140-293-36	US-09-764-864-1018	US-08-976-063C-36	US-09-815-242-13033	US-09-764-891-5242	US-09-925-299-1271	US-09-925-299-1271	us-09-764-869-1068	US-10-091-504-1068	us-09-867-550-156	US-09-764-877-1147	US-09-840-298-12	US-09-840-298-11	US-09-840-298-10	US-09-989-920-192	US-09-764-877-1962	US-09-865-294-44	US-09-747-802-52	US-10-078-770-138	-10-103-313	US-09-764-891-5030
Sequence 992, App	Sequence 1191, Ap	Sequence 28, Appl		Sequence 37, Appl	Sequence 36, Appl	Sequence 1018, Ap	Sequence 36, Appl	Sequence 13033, A	Sequence 5242, Ap	Sequence 1271, Ap	Sequence 1271, Ap	Sequence 1068, Ap			Sequence 1147, Ap	Sequence 12, Appl	-	Sequence 10, Appl	Sequence 192, App	Sequence 1962, Ap	Sequence 44, Appl	Sequence 52, Appl	Sequence 138, App	Sequence 503, App	Sequence 5030, Ap

ALIGNMENTS

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; Sequence 6, Application US/09809517A
; Patent NO. US20020034733A1
; GENERAL INFORMATION:
; APPLICANT: Lohning, Corinna
; TITLE OF INVENTION: No. US20020034733A1el methods for displaying (poly)peptides/pr
; TITLE OF INVENTION: particles via disulfide bonds
; FILE REFERENCE: MORPHO/11
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US-09-809-517A-6
                                                                                                                                               RESULT 2
US-10-104-218-5
                                                                                                                                                                                                                                                                                                                                                                                                                                 OTHER INFORMATION: Description of Artificial Sequence: synthetic module US-09-809-517A-6
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                                                                       Sequence 5, Application US/10104218 Patent No. US20020177196A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQ ID NO 6
LENGTH: 10
TYPE: PRP
ORGANISM: artificial sequence
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                     Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/809,517A CURRENT FILING DATE: 2001-03-15 PRIOR APPLICATION NUMBER: EP 99114072.4 PRIOR FILING DATE: 1999-07-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER: EP 00103551.8
PRIOR FILING DATE: 2000-02-18
NUMBER OF SEQ ID NOS: 41
APPLICANT: MAIER, Thomas
APPLICANT: GAEBERT, Carsten
TITLE OF INVENTION: PROCESS FOR PREPARING NON-PROTEINOGENIC L-AMINO ACIDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FEATURE:
                                                                                                                                                                                                                                                                                      108 SAWSHPOFEK 117
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                                                                                             Sequence 8, Application US/10001934 Publication No. US20030032782A1 GENERAL INFORMATION:
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                 APPLICANT: NAGY, ZOLTAN
TITLE OF INVENTION: HUMAN PEPTIDES/PROTEINS CAUSING OR LEADING TO THE
TITLE OF INVENTION: KILLING OF CELLS INCLUDING LYMPHOID TUMOR CELLS
FILE REFERENCE: GPCG-P01-003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/10/208,357
CURRENT FILING DATE: 2002-07-30
PRIOR APPLICATION NUMBER: US/09/619,103
PRIOR FILING DATE: 2000-07-19
PRIOR APPLICATION NUMBER: 60/145,834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR FILING DATE: 1999-07-27
NUMBER OF SEQ ID NOS: 26
SOFTWARE: FastSEQ for Windows Version 4.0
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CURRENT FILING DATE: 2002-03-22
PRIOR APPLICATION NUMBER: German No. US20020177196A1 101 16 881.0
PRIOR FILING DATE: 2001-04-04
PRIOR APPLICATION NUMBER: German No. US20020177196A1 101 21 515.0
PRIOR APPLICATION NUMBER: German No. US20020177196A1 101 21 515.0
PRIOR FILING DATE: 2001-05-03
 CURRENT APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Wagner, Richard
TITLE OF INVENTION: Peptide Acceptor Ligation Methods
FILE REFERENCE: 50036/031002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Kurz, Markus APPLICANT: Lohse, Pete
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILE REFERENCE: MAIER, T. ET AL.-2
                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: PEPTIDE LOCATION: (1)..(8) OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                         OTHER INFORMATION: designed sequence
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les 8; Conserv
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mes 8; Conserv
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US/10/001,934
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0; Mismatches
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NO. 3.4e+05;
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b. 3.4e+05;
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US-10-026-578B-9
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US-10-001-934-8
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Best Local Similarity
"hes 8; Conserv
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APPLICANT: IBA (GmbH)
APPLICANT: Schmidt, Thomas
APPLICANT: Schmidt, Thomas
TITLE OF INVENTION: Sequentially Arranged Streptavidin-Binding Modules as Affinity
FILE REFERENCE: 100810.01US1
CURRENT APPLICATION NUMBER: US/10/026,578B
CURRENT FILING DATE: 2002-11-11
PRIOR APPLICATION NUMBER: DE 101 13 776.1
PRIOR FILING DATE: 2001-03-21
PRIOR FILING DATE: 2001-03-21
PRIOR FILING DATE: 2001-10-12
                                                                                                                                                                                                                                              Sequence 9, Application US/10026578B Publication No. US20030083474A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
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SEQ ID NO 2
LENGTH: 8
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SOFTWARE: PATENTIN VET. 2.1
SEQ ID NO 8
LENGTH: 8
                                                                                                                                                                                                                          GENERAL INFORMATION:
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APPLICANT: Schmidt, Thomas
APPLICANT: Schmidt, Thomas
TITLE OF INVENTION: Sequentially Arranged Streptavidin-Binding Modules as Affinity
FILE REFERENCE: 100810.01US1
CURRENT APPLICATION NUMBER: US/10/026,578B
CURRENT FILING DATE: 2002-11-11
PRIOR APPLICATION NUMBER: DE 101 13 776.1
PRIOR APPLICATION NUMBER: DE 101 13 776.1
PRIOR FILING DATE: 2001-03-21
PRIOR FILING DATE: 2001-03-21
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PRIOR FILING DATE: 2001-10-12
NUMBER OF SEQ ID NOS: 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT ORGANISM: artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FEATURE:
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100.0%; Pr
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100.0%;
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b; Pred. No. 3.4
0; Mismatches
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Pred. No.
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No. 3.4e+05;
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RESULT 7
US-10-174-368A-7
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US-09-809-517A-9
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                                                                     Sequence 9, Application US/09809517A
Patent No. US20020034733A1
GENERAL INFORMATION:
APPLICANT: Lohning, Corinna
TITLE OF INVENTION: No. US20020034733A1el methods for displaying (poly)peptides/prote
TITLE OF INVENTION: particles via disulfide bonds
FILE REFERENCE: MORPHO/11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 7, Application US/10174368A Publication No. US20030092031A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SOFTWARE: PatentIn version 3.1 SEQ ID NO 7
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APPLICANT: Gite, Sadanand
APPLICANT: Gite, Sadanand
APPLICANT: Olighik, Jerzy
TITLE OF INVENTION: Methods for the Detection, Analysis and Isolation of Nascent Pro
FILE REFERENCE: AMBER-07145
CURRENT APPLICATION NUMBER: US/10/174,368A
CURRENT FILING DATE: 2002-06-18
CURRENT FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: 10/049,332
PRIOR FILING DATE: 2002-06-21
PRIOR APPLICATION NUMBER: PCT/US00/23233
PRIOR FILING DATE: 2000-08-23
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                                      CURRENT APPLICATION NUMBER: US/09/809,517#
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: 09/382,736 PRIOR FILING DATE: 1999-08-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: PatentIn version
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TYPE: PRT
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ORGANISM: Artificial Sequence
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NAME/KEY: misc_feature
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2001-03-15
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; OTHER INFORMATION: Description of Artificial Sequence: synthetic module US-09-809-517A-9
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NAME/KEY: misc_feature

; OTHER INFORMATION: Synthetic

US-09-973-145-7
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US-09-983-067-3
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             Sequence 3, Application US/09983067
Patent No. US20020123101A1
GENERAL INFORMATION:
APPLICANT: INOUE, Akio
APPLICANT: SHIMIZU, Yoshihiro
APPLICANT: UEDA, Takuya
TITLE OF INVENTION: Process for Producing Peptides By Using In Vitro
TITLE OF INVENTION: Transcription/Translation System
FILE REFERENCE: 1752-0151P
CURRENT APPLICATION NUMBER: US/09/983,067
CURRENT FILING DATE: 2001-10-23
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Best Local Similarity
Thes 8; Conserv
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SOFTWARE: PatentIn version 3.1
SEQ ID NO 7
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SOFTWARE: PatentIn version 3.0
SEQ ID NO 9
LENGTH: 8
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Best Local :
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APPLICANT: Gite, Sadanand
APPLICANT: Olejnik, Jerzy
TITLE OF INVENTION: N-Terminal and C-Terminal Markers in Nascent Proteins
FILE REFERENCE: AMBER-06819
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CURRENT FILING DATE: 2001-10-09
PRIOR APPLICATION NUMBER: 09/382,950
PRIOR FILING DATE: 1999-08-25
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PRIOR APPLICATION NUMBER: JP 294795/2001
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100.0%; Pr
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100.0%; Pred. No. 3.
tive 0; Mismatches
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US-09-809-517A-33
Sequence 33, Application US/09809517A
Patent No. US20020034733A1
GENERAL INFORMATION:
APPLICANT: Lohning, Corinna
TITLE OF INVENTION: No. US2002003473:
TITLE OF INVENTION: particles via d.
                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
""" hes 8; Conserv
                                                                                                                                                     RESULT 12
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US-09-809-517A-30
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LENGTH: 21
TYPE: PRT
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APPLICANT: Lohning, Corinna
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Best Local Similarity
Matches 8; Conser
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TITLE OF INVENTION: No. US20020034733Alel methods for displaying (poly)peptides/prote
TITLE OF INVENTION: particles via disulfide bonds
FILE REFERENCE: MORPHO/11
CURRENT APPLICATION NUMBER: US/09/809,517A
CURRENT FILING DATE: 2001-03-15
PRIOR APPLICATION NUMBER: EP 99114072.4
PRIOR FILING DATE: 1999-07-20
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OTHER INFORMATION: Schm:
OTHER INFORMATION: Strep
OTHER INFORMATION: strep
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PRIOR FILING DATE: 2001-07-27
PRIOR APPLICATION NUMBER: JP 6910/2001
PRIOR FILING DATE: 2001-01-15
PRIOR PELICATION NUMBER: JP 401417/2000
PRIOR PILING DATE: 2000-12-28
NUMBER OF SEQ ID NOS: 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: EP 00103551.8
PRIOR FILING DATE: 2000-02-18
NUMBER OF SEQ ID NOS: 41
SOFTWARE: PatentIn version 3.0
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Corinna No. US20020034733Alel methods for displaying (poly)peptides/prote particles via disulfide bonds
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Pred. No.
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US-10-026-578B-3
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LENGTH: 24
TYPE: PRT
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LENGTH: 22
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APPLICANT: Schmidt, Thomas
TITLE OF INVENTION: Sequentially Arranged Streptavidin-Binding Modules as Affinity
FILE REFERENCE: 100810.01US1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILE REFERENCE: MORPHO/11
CURRENT APPLICATION NUMBER: US/09/809,517A
CURRENT FILING DATE: 2001-03-15
PRIOR APPLICATION NUMBER: EP 99114072.4
PRIOR FILING DATE: 1999-07-20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: PCT/EP01/11846
PRIOR FILING DATE: 2001-10-12
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin version 3.1
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PRIOR FILING DATE: 2001-03-21
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                                                                                                                                                             NAME/KEY: MISC_FEATURE LOCATION: (12)..(12) OTHER INFORMATION: X represents a single amino acid at the
                                                                                   OTHER INFORMATION: X represents a
                                                                                                                                                                                                                                                 LOCATION: (11)..(11)
OTHER INFORMATION: X represents a single
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OTHER INFORMATION: x represents
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                                         NAME/KEY: MISC_FEATURE
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ION: (14)..(14)
INFORMATION: X represents a single amino acid
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RESULT 14
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TITLE OF INVENTION: Sequentially Arranged Streptavidin-Binding Modules as Affinity Ta
FILE REFERENCE: 100810.01US1
CURRENT APPLICATION NUMBER: US/10/026,578B
CURRENT FILING DATE: 2002-11-11
PRIOR APPLICATION NUMBER: DE 101 13 776.1
PRIOR PRIOR APPLICATION NUMBER: DE 101 13 776.1
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: PCT/EP01/11846
PRIOR FILING DATE: 2001-10-12
NUMBER OF SEQ ID NOS: 14
SOFTWARE: Patentin version 3.1
SEQ ID NO 4
LENGTH: 24
TYPE: PRT
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APPLICANT: IBA (GmbH)
APPLICANT: Schmidt,
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Best Local
                                                                                                                              NAME/KEY: MISC_FEATURE LOCATION: (13)..(13) OTHER INFORMATION: X represents
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                                                            LOCATION: (14)..(14)
OTHER INFORMATION: X represents
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LOCATION: (10)...(10)
OTHER INFORMATION: X represents a single
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LOCATION: (9)..(9)
OTHER INFORMATION: X represents
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NAME/KEY: MISC_FEATURE
LOCATION: (11)..(11)
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   LOCATION: (15)..(15)
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OTHER INFORMATION: Artificial Sequence represents peptide binding module
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OTHER INFORMATION: X represents a
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OTHER INFORMATION: X represents a single amino acid at the position indicated
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US-09-809-517A-31
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                                                                                                                                                                                                        SEQ ID NO 31
LENGTH: 24
TYPE: PRT
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patent No. US20020034733A1
GENERAL INFORMATION:
APPLICANT: Lohning, Corinna
TITLE OF INVENTION: No. US20020034733A1e1 methods for displaying (poly)peptides/pr
TITLE OF INVENTION: particles via disulfide bonds
FILE REFERENCE: MORPHO/11
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Best Local
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                                                                                                                                                                                                                                                          SOFTWARE: PatentIn version 3.0
                                                                                                                                                                                    ORGANISM: artificial sequence
                                                                                                                                                    OTHER INFORMATION: Description
                                                                                                                                                                        FEATURE:
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OTHER INFORMATION: X represents a
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OTHER INFORMATION: X represents a
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OTHER INFORMATION: X represents a single amino acid
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17 WSHPQFEK
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Pred. No. 0.2;
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Search completed: May 28,

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Job time : 58 secs

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/cgn2_6/ptodata/1/paa/US084_COMB.pep: *
/cgn2_6/ptodata/1/paa/US085_COMB.pep: *
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US-09-977-137A-9	US-09-977-137A-8	US-09-977-137A-7	US-09-977-137A-5	US-09-977-137A-12	US-09-977-137A-4	ID
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Sequence 359, App Sequence 359, App	e 10064, e 20227, e 15593,	e 22, e 19, e 1007 e 26, e 27, e 6154	31, 34, 19, 24, 26, 26, 26, 26, 26, 26, 26, 26, 26, 26	3958879652356601888	equence 10,

ALIGNMENTS

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US-09-977-137A-4
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US-09-977-137A-4
; Sequence 4, Application US/09977137A
; GENERAL INFORMATION:
; APPLICANT: Summers, Anne O.
; APPLICANT: Caguiat, Jonathan
                                                                                                                                                                                                                                                                  APPLICANT: Caguiat, Jonathan
TITLE OF INVENTION: Metal Binding Proteins, Recombinant Host Cells and
TITLE OF INVENTION: Methods
FILE REFERENCE: 79-00
CURRENT PELLING NUMBER: US/09/977,137A
CURRENT FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: US 60/240,465
PRIOR FILING DATE: 2000-10-12
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 4
LENGTH: 117
                                                 Best Loc
Matches
                                                                                                  Query Match
                                                                                                                                                     TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
OTHER INFORMATION: Description of Artificial Sequence: chelon
                                              Match 100.0%; Score 117; DB 23; Local Similarity 100.0%; Pred. No. 3.3e-113; tes 117; Conservative 0; Mismatches 0;
1 MTHCEEASSLAEHKLKDVREKMADLARMETVLSELVCACHARKGNVSCPLIASLQGSSGT 60
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GENERAL INFORMATION:
APPLICANT: Summers, Anne O.
APPLICANT: Cagulat, Jonathan
TITLE OF INVENTION: Metal Binding Proteins, Recombinant Host Cells
TITLE OF INVENTION: Methods
FILE REFERENCE: 79-00
CURRENT APPLICATION NUMBER: US/09/977,137A
CURRENT FILING DATE: 2001-10-12
                                                                                                                                                                                                                                                                                                                                                                                      Sequence 5, Application US/09977137A
GENERAL INFORMATION:
APPLICANT: Summers, Anne O.
APPLICANT: Caguiat, Jonathan
                                                                                             Query Match
                                                                                                                                                                                                                            SEQ ID NO 5
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PRIOR APPLICATION NUMBER: US 60/240,465
PRIOR FILING DATE: 2000-10-12
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: Metal Binding Proteins, Recombinant Host Cells and FILE OF INVENTION: Methods
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ORGANISM: Artificial Sequence
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US-09-977-137A-7
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                                                                                                                  RESULT 6
                                                        Sequence 9, Application US/09977137A GENERAL INFORMATION:
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SOFTWARE: PATENTIN VET. 2.0
SEQ ID NO 8
LENGTH: 117
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NUMBER OF SEQ ID NOS: 18
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION NUMBER: US/09/977,137A CURRENT FILING DATE: 2001-10-12 PRIOR APPLICATION NUMBER: US 60/240,465 PRIOR FILING DATE: 2000-10-12
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CURRENT FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: US 60/240,465
APPLICANT: Summers, Anne O.
APPLICANT: Caguiat, Jonathan
TITLE OF INVENTION: Metal Binding Proteins,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Metal Binding Proteins, TITLE OF INVENTION: Methods FILE REFERENCE: 79-00
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Pred. No.
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    Recombinant Host Cells and
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GENERAL INFORMATION:
APPLICANT: Summers, Anne O.
APPLICANT: Caguiat, Jonathan
TITLE OF INVENTION: Metal Binding Proteins, Recombinant Host Cells and
TITLE OF INVENTION: Methods
FILE REFERENCE: 79-00
                                                                                                                                                                                                                                               Sequence 11, Application US/09977137A GENERAL INFORMATION:
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Best Local Similarity
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SEQ ID NO 10
LENGTH: 117
TYPE: PRT
SEQ ID NO 11
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                                                       CURRENT APPLICATION NUMBER: US/09/977,137A
CURRENT FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: US 60/240,465
PRIOR FILING DATE: 2000-10-12
                                                                                                                                        APPLICANT: Caguiat, Jonathan TITLE OF INVENTION: Metal Binding Proteins, Recombinant Host Cells and TITLE OF INVENTION: Methods
FILE REFERENCE: 79-00
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PRIOR FILING DATE: 2000-10-12
NUMBER OF SEQ ID NOS: 18
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CURRENT APPLICATION NUMBER: US/09/977,137A
CURRENT FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: US 60/240,465
PRIOR FILING DATE: 2000-10-12
NUMBER OF SEQ ID NOS: 18
                 NUMBER OF SEQ ID NOS: 18 SOFTWARE: PatentIn Ver.
                                                                                                                                                                                                         APPLICANT: Summers, Anne O. APPLICANT: Caguiat, Jonath
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: PRT
ORGANISM: Artificial Sequence
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nes 57; Conser
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100.0%; Pr
100.0%; O;
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Pred. No.
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9.8e-51;
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                                                                                                                                                                      SEQ ID NO 5823
LENGTH: 220
TYPE: PRT
                                                                      Matches
                                                                                    Query Match
Best Local Similarity
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Best Local Similarity
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                                                                                                                                                                                                                                                                         APPLICANT: Keith G. Weinstock et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ENTEROBACTE
TITLE OF INVENTION: CLOACAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.135
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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                                                                                                                                                                                                                                           CURRENT FILING DATE:
                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/252,6918
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NUMBER OF SEQ ID NOS: 18
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TYPE: PRT
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156 THCEEASSLAEHKLKDVREKMADLARMETVLSELVCACHARKGNVSCPLIASLQG 210
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les 55; Conserv
                                 2 THCEEASSLAEHKLKDVREKMADLARMETVLSELVCACHARKGNVSCPLIASLQG
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Pred. No.
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2.1e-48;
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9.8e-51;
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RESULT 13
US-09-252-691-6093
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US-09-489-039A-11501
; Sequence 11501, Application US/09489039A
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PRIOR APPLICATION NUMBER: US 60/074,787;
PRIOR FILING DATE: 1998-02-18
NUMBER OF SEQ ID NOS: 11326
SEQ ID NO 5823
LENGTH: 220
TYPE: DDT
                                 CURRENT APPLICATION NUMBER: US/09/252,691B
CURRENT FILING DATE: 1999-02-18
NUMBER OF SEQ ID NOS: 11324
SEQ ID NO 6093
LENGTH: 255
TYPE: PRT
                                                                                                                                              Sequence 6093, Application US/09252691B
GENERAL INFORMATION:
APPLICANT: Keith G. Weinstock et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID
TITLE OF INVENTION: CLOACAE FOR DIAGNOSTICS AND
FILE REFERENCE: 107196.135
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APPLICANT: Gary Breton et. al
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO KLEBSIELLA
TITLE OF INVENTION: PNEUMONIAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 2709.2004001
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LENGTH: 221
TYPE: PRT
ORGANISM: Klebsiella pneumoniae
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Best Local
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TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ENTEROBACTER
TITLE OF INVENTION: CLOACAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.135
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ORGANISM: Enterobacter cloacae
FEATURE:
                 ORGANISM: Enterobacter cloacae
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les 55; Conserv
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100.0%; Pred. No.
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2.1e-48;
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               UNSURE
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; NAME/KEY: UNSURE
; LOCATION: (58)
US-09-252-691-6093
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SEQ ID NO 6093
LENGTH: 255
TYPE: PRT
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APPLICANT: Keith G
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Best Local Similarity
                                                                                                                                                                                                                                                    PRIOR FILING DATE: 1998-07-24
PRIOR APPLICATION NUMBER: US 60/074,787
PRIOR FILING DATE: 1998-02-18
PRIOR FILING DATE: 1998-01-19
                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/252,691C CURRENT FILING DATE: 1999-02-18
                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Keith G. Weinstock et al.
TITLE OF INVENTION: NUCLEIC ACID AND AMINO ACID SEQUENCES RELATING TO ENTEROBACTE
TITLE OF INVENTION: CLOACAE FOR DIAGNOSTICS AND THERAPEUTICS
FILE REFERENCE: 107196.135
                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION NUMBER:
                                                                                                                                                                                 ORGANISM: Enterobacter cloacae
                                                                                                                                               NAME/KEY: UNSURE
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Sequence 6, Application US/09977137A
GENERAL INFORMATION:
APPLICANT: Summers, Anne O.
APPLICANT: Caguiat, Jonathan
TITLE OF INVENTION: Methal Binding Proteins, Recombinant Host Cells and
TITLE OF INVENTION: Methods
FILE REFERENCE: 79-00
CURRENT APPLICATION NUMBER: US/09/977,137A
CURRENT FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: US 60/240,465
PRIOR FILING DATE: 2000-10-12
NUMBER OF SEQ ID NOS: 18
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 6
LENGTH: 118
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
COTHER INFORMATION: Description of Artificial Sequence: chelon
US-09-977-137A-6
Search completed: May 28, 2003, 10:48:43 Job time: 332 secs
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US-09-977-137A-6
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                                                                                                                                       Query Match 41.0%; Score 48; DB 23; Length 118; Best Local Similarity 100.0%; Pred. No. 2.3e-41; Matches 48; Conservative 0; Mismatches 0; Indels
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Maximum Match 100%
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Maximum DB
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Perfect score:
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    Issued_Patents_NA:*
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/cgn2_6/ptodata/1/ina/5B_COMB.seq:*
/cgn2_6/ptodata/1/ina/6B_COMB.seq:*
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/cgn2_6/ptodata/1/ina/FCTUS_COMB.seq:*
/cgn2_6/ptodata/1/ina/Fackfiles1.seq:*
US-09-232-279-1
US-08-08-8847-1
US-08-08-558-1
US-09-244-796-17
4 US-09-103-840A-2
4 US-09-103-840A-2
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US-08-676-967-5
US-08-676-974-5
US-08-676-974-5
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US-09-199-637A-160
US-08-9199-637A-114
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US-09-889-595-4
US-08-818-112-12
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                                                  Sequence 1, Appli
Sequence 1, Appli
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Sequence 1, Appli
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Sequence
Sequence
Sequence
                  4, Appli
12, Appl
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RESULT 2 US-08-682-847-1

Sequence 1, Application US/08682847
Patent No. 5858989
GENERAL INFORMATION:

APPLICANT: BABIUK, LORNE
APPLICANT: VAN DEN HURK, SYLVIA
APPLICANT: ZAMB, TIM
APPLICANT: FITZPATRICK, DAVID

ZAMB, TIM FITZPATRICK, DAVID

TITLE OF INVENTION: RECOMBINANT BOVINE HERPESVIRUS TYPE

Db	Qy	DЬ	Qγ	Db	οv	Qу	3 13 10	RESULT US-09-1 Seque Pates GENES ATIT FILI FILI CURR CURR SOF SEQ LE LE TTT TTT TTT TTT TTT TTT TTT TTT T		0
							Query M Best Lo Matches	SULT 1 patent No. 6 general INFO APPLICANT TITLE OF IN FILE REFERE CURRENT FIL NUMBEROF SOFTWARE: SEQ ID NO 1 LENGTH: 27 TYPE: DNA ORGANISM: 5-09-232-279-		22555555555555555555555555555555555555
2091	189	2031	129		69	9 (atch cal 10	ULT 1 09-232-279-1 equence 1, Appl atent No. 63764 ENERAL INFORMAT APPLICANT: Aud TITLE OF INVENT FILE REFERENCE: CURRENT APPLICA CURRENT FILING NUMBER OF SEQ I SOFTWARE: Pate EQ ID NO 1 LENGTH: 2799 TYPE: DNA ORGANISM: BOVI 09-232-279-1		00000000000000000000000000000000000000
GGTGATCAGCACCTTTGTGGAC	GGAGGCCAGCAGCCTGGCCGAA	GGACTACGTGTACTACGAGAAC	GGGGAATGTTTCCTGCCCGTTG	GGGCCGCGAGCTCGTGGAGCCTGCACCGCCAACCACAAGCGCTACTTCCGCTTTGGCGC	CGACTTGGCGCGCATGGAAACC	CTGCGAGGAGGCCAGCAGCCTGGCCGAACACAAGCTCAAGGACGTGCGCGAGAAGATGGC	11.3%; milarity 47.6%; Conservative (ication US/0923227 73 ION: ION: POLYNUCLEOTI ION: PREATING BOV 454313-2250 TION NUMBER: US/09 DATE: 1999-01-15 D NOS: 19 ntin Ver: 2.1 ne herpesvirus 2		9.5 1155 4 US-0 9.5 1171 4 US-0 9.5 5058 4 US-0 9.5 1151 1 US-0 9.5 2943 1 US-0 9.5 3027 2 US-0 9.5 3760 3 US-0 9.4 3760 3 US-0 9.4 3760 3 US-0 9.3 2505 1 US-0 9.3 2505 1 US-0 9.3 2505 1 US-0 9.3 2713 3 US-0 9.3 3472 6 5244 9.3 31236 1 US-0
GGTGATCAGCACCTTTGTGGACCTAAACCTCACGGTTCTGGAGGA	GGAGGCCAGCAGCCTGGCCGAACACAAGCTCAAGGACGTGCGCGA	GGACTACGTGTACTACGAGAACTACGCGTACGTGCGGGGGTCCCGGTCGCGGAGCTGGA	GGGGAATGTTTCCTGCCCGTTGATCGCGTCACTACAGGGATCCTCAGGCACCCACTGCGA	TGCACCGCCAACCACAAGCGCTI	CGACTTGGCGCGCATGGAAACCGTGCTGTCTGAACTCGTGTGCGCCTGCCATGCACGAAA	CTGCGAGGAGGCCAGCAGCAGCCTGGCCGAACAAACCTCAAGGACGTGCGCGAGAAAGATGGC 	Score 36.2; DB 4; Length Pred. No. 0.28; Indels	VACCINE FORMULA, E RESPIRATORY DISE 32,279	ALIGNMENTS	US-09-056-556-12 US-09-072-596-12 US-09-754-250-1 US-09-889-595-1 US-08-807-044-2 US-08-042-747A-7 US-08-680-326-23 US-09-773-816-1 US-09-270-984A-1 US-09-372-422A-29 US-09-372-422A-29 US-08-458-819-7 US-08-804-439A-13 US-08-720-229-13 US-08-720-229-13
A 2135	A 233	CGCTCGCGGAGCTGGA 2090	CAGGCACCCACTGCGA 188	N	CCTGCCATGCACGAAA 128	TGCGCGAGAAGATGGC 68	th 2799; els	PARTICULARLY FOR		Sequence 12, Appl Sequence 12, Appl Sequence 1, Appli Sequence 2, Appli Sequence 7, Appli Sequence 7, Appli Sequence 1, Appli Sequence 1, Appli Sequence 1, Appli Sequence 7, Appli Sequence 7, Appli Sequence 7, Appli Sequence 13, Appli Sequence 11, Appli

CORRESPONDENCE ADDRESS:
ADDRESSEE: MORRISON & FOERSTER
STREET: 755 PAGE MILL ROAD

STREET: 755 PAGI

TITLE OF INVENTION: NUMBER OF SEQUENCES:

POLYPEPTIDES AND VACCINES

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US-08-035-558-1
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; LOCATION:
US-08-682-847-1
                                                                                                                                                                             Sequence 1, Application US/08035558 Patent No. 5462734 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 107; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: PARK, FREDDIE K.
REGISTRATION NUMBER: 35,636
REFERENCE/DOCKET NUMBER: 2931
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
TELEPAX: (415) 494-0792
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INFORMATION FOR SEQ ID NO:
                                     NUMBER OF SEQUENCES: 3
CORRESPONDENCE ADDRESS:
ADDRESSEE: Quarles a
                                                                                                 APPLICANT: Letchworth, Geoffr
APPLICANT: Israel, Barbara A.
TITLE OF INVENTION: HERPESVIR
TITLE OF INVENTION: OF USING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: (= 706141
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: FILING DATE: 12-JUL
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FIRST WISCONSIN PLAZA
                    E: Quarles and Brady P.O BOX 2113
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                                                                                                                                                      Letchworth, Geoffrey J.
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                                                                                                 HERPESVIRUS VACCINE AND METHOD OF USING SAME
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Pred. No. 0.29;
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RESULT 4

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Best Local Similarity 47.6%;
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[NFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE:
HYPOTHETICAL: r
ANTI-SENSE: no
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Microsoft Word 4.0 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (608)251-5000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 02-NOV-1990 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 424
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                    PAGES:
DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                           AUTHORS: Nelson, Randy
AUTHORS: Smith, Michael
TITLE: Sequence of a Bovine Herpesvirus Type-1 etc.
JOURNAL: Virology
VOLUME: 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: coding sequence for gI glycoprotein LOCATION: 379 to 3165
IDENTIFICATION METHOD: sequence analysis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY:
LOCATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM: bovine herpervirus-1 INDIVIDUAL ISOLATE: P8-2 strain
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APPLICATION NUMBER: 07/60
PTITING DATE: 02-NOV-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: Apple Macintosh
OPERATING SYSTEM: Macinto
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AUTHORS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME:
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                                                                                                                                                                                                                                                                                                                                                                                                    RELEVANT RESIDUES IN SEQ ID NO:
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                                                                            2400
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                                                                                                                                                                                                                                                                                                        107;
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                       GGAGGCCAGCCTGGCCGAACACACAGCTCAAGGACGTGCGCGA 233
GGTGATCAGCACCTTTGTGGACCTAAACCTCACGGTTCTGGAGGA 2504
                                                                          GGACTACGTGTACTACGAGAACTACGCGTACGTGCGGCGGGTCCCGCTCGCGGAGCTGGA
                                                                                                             GGGGAATGTTTCCTGCCCGTTGATCGCGTCACTACAGGGATCCTCAGGCACCCACTGCGA 188
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Pred. No. 0.3;
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TITLE OF INVENTION: EUECTION OF PROTEINS USINTITLE OF INVENTION: FUSIONS
FILE REFERENCE: 00786/350003
CURRENT APPLICATION NUMBER: US/09/007,005B
CURRENT FILING DATE: 1998-01-14
EARLIER APPLICATION NUMBER: 60/035,963
EARLIER FILING DATE: 1997-01-27
EARLIER FILING DATE: 1997-01-27
EARLIER APPLICATION NUMBER: 60/064,491
EARLIER FILING DATE: 1997-11-06
NUMBER OF SEQ ID NOS: 33
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 17
LENGTH: 289
                                                                  APPLICANT: SZOSTAK, Jack W.

APPLICANT: Roberts, Richard W.

APPLICANT: Liu, Rihe

TITLE OF INVENTION: SELECTION OF PROTEINS USING RNA-PROTEIN

TITLE OF INVENTION: FUSIONS

FILE REFERENCE: 00786/350007

CURRENT APPLICATION NUMBER: US/09/244,796

CURRENT FILING DATE: 1999-02-05

EARLIER APPLICATION NUMBER: 60/055,963

EARLIER FILING DATE: 1997-01-27

EARLIER FILING DATE: 1997-01-06

EARLIER FILING DATE: 1997-01-06

EARLIER APPLICATION NUMBER: 60/064,491

EARLIER APPLICATION NUMBER: 09/007,005

EARLIER APPLICATION NUMBER: 09/007,005
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; Sequence 17, Application US/09007005B
; Patent No. 6258558
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NUMBER OF SEQ ID NOS: 33
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 17
                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 17, Application US/09244796 Patent No. 6281344
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LOCATION: (1)...(289)
OTHER INFORMATION: n = A,T,C or
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ORGANISM: Artificial Sequence
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Pred. No. 0.3;
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; NAME/KEY: misc_feature
; LOCATION: (1)...(289)
; OTHER INFORMATION: n = A,T,C
US-09-244-796-17
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APPLICANT: WHITE, Owen R.
APPLICANT: FRASE, Claire M.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN
TITLE OF INVENTION: TUBERCULOSIS
FILE REFERENCE: 24366-2007.00
CURRENT APPLICATION UNMBER: US/99/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ. ID NOS: 2
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LENGTH: 4403765
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                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                Query Match
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                                                                                                                                                                                                                                                                                                                                                          OTHER INFORMATION: CDC 1551
OTHER INFORMATION: "n" bases at various positions throughout the sequence OTHER INFORMATION: represent a, t, c or g
                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                            TYPE: DNA ORGANISM: Mycobacterium tuberculosis
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TYPE: RNA
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                                                                                                                                                                                                                                                                          Local Similarity
                                                                                                                                                                      791022 GTGGTCGGTGGCGGGATGGCCGGCAAGGTCATGAAGGTGCGCGGCAAGATCGCCGCGGGC 791081
791142 GCGCCCTGGTCGTCGCCGCATTCGGCGGACATATCGTCTGGCTGTCGGGACGGCTCGGCC
                                                                                  791082 GCGCCCATCGCCGAAGTGTTAGACCAAACTCAGGCCTAGAGCTGACCTAGGTGGCAGCGG 791141
                                       136 GTTTCCTGCCCGTTGATCGCGTCACTACAGGGATCCTCAGGCACCCACTGCGAGGAGGCC 195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        213 RNRNRSRCRARGRCRURGRCRGRURARARCRURCRURURGR 253
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               220 AAGGACGTGCGCGAGAAGATGGCCGACTTGGCGCGCGCATGGA 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          153 RNRNRSRNRNRSRNRNRSRNRNRSRNRNRSRNRNRSRNRNRSRNRNRSRNRNRSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100 GAACTCGTGTGCGCCTGCCATGCACGAAAGGGGAATGTTTCCTGCCCGTTGATCGCGTCA 159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          93 RNRNRSRNRNRSRNRNRSRNRNRSRNRNRSRNRNRSRNRNRSRNRNRSRNRNRSRNRNRS 152
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                                                                                                                                                                                                            16 GAGGCCAGCCTGGCCGAACACAAGCTCAAGGACGTGCGCGAGAAGATGGCCGACTTG 75
                                                                                                                                                                                                                                                        96;
                                                                                                                              GCGCGCATGGAAACCGTGCTGTCTGAACTCGTGTGCGCCTGCCATGCACGAAAGGGGAAT 135
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48.2%;
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                                                                                                                                                                                                                                                      Score 34.2; DB 4; Length 4
Pred. No. 4.1;
0; Mismatches 103; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 35.4;
Pred. No. 0.3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FOR STRAIN ANALYSIS
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                                                                                                                                                                                                                                                                                                Length 4403765;
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; ORGANISM: Mycobacterium tuberculosis
; OTHER INFORMATION: H37Rv
US-09-103-840A-1
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                                                                                                                                                                                                                                                                                                                                           Sequence 3, Application Patent No. 5824513 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 1, Application US/09103840A Patent No. 6294328
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CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: VENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
TITLE OF INVENTION: TUBERCULOSIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: FLEISCHMAN, Robert D.
APPLICANT: WHITE, Owen R.
APPLICANT: FRASER, Claire M.
APPLICANT: VENTER, John C.
             ZIP: 60064-3500
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 4411529
                                                                                                                                                                                     CORRESPONDENCE ADDRESS:
ADDRESSEE: Edward H. Gorman
                                                                                                                                                                                                                                              TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                      APPLICANT:
                                                                                                                                                                                                                                                                                                                         APPLICANT:
                                                                                                                                                                                                                               NUMBER OF SEQUENCES:
                                                                                                                                STREET: Abbott Laboratories D377/AP6D-2 One Abbott STREET: Park Rd CITY: Abbott Park
COMPUTER: IBM PC OPERATING SYSTEM:
                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                789240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   789060 GTGGTCGGTGGCGGGATGGCCGGCAAGGTCATGAAGGTGCGCGGCAAGATCGCCGCGGGC 789119
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les 96; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 196 AGCAGCCTGGCCGAACACA 214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             76 GCGCGCATGGAAACCGTGCTGTCTGAACTCGTGTGCGCCTGCCATGCACGAAAGGGGGAAT 135
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AGCGCGCCGGCCGCACGCA 789258
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PC-DOS/MS-DOS
                                                                                                                                                                                                                               Erythromycin
27
                                                                                                                                                                                                                                                              Recombinant DNA Method for Producing
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Pred. No. 4.1;
0; Mismatches 103;
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TELEFAX: 708-938-2623
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 20235 base pai
                     FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Danckers, Andreas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FEATURE:
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ANTI~SENSE: NO
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LOCATION:
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LOCATION:
                                  OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                           OTHER INFORMATION: /function= "approximate OTHER INFORMATION: beta-ketoacylACPsynhase
                                                                                                                                                                                                                         OTHER INFORMATION: OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                    NAME/KEY: misc_feature
LOCATION: 3406..3921
OTHER INFORMATION: /function= "approximate span of
OTHER INFORMATION: beta-ketoreductase domain of module
                                                                     NAME/KEY: misc_feature LOCATION: 6054..7026
                                                                                                                                                               NAME/KEY: misc_feature LOCATION: 4471..5847
                                                                                                                                                                                                                                                         NAME/KEY: misc_feature LOCATION: 4471..10722
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OTHER INFORMATION: /fur OTHER INFORMATION: beta
 NAME/KEY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Danckers, Andreas M
REGISTRATION NUMBER: 3265
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misc_feature
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                                  /function= "approximate span of
acyltransferase domain of module 4"
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module 4"
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module 3"
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/product= "eryA ORF2 encoding modules 3 & 4 for 6-deoxyerythronolide B"
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domain of module
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NAME/KEY: misc_feat
LOCATION: 14062..14
OTHER INFORMATION:
OTHER INFORMATION:
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                                                      LOCATION: 19149..1
OTHER INFORMATION:
OTHER INFORMATION:
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LOCATION: 16768..17721
OTHER INFORMATION: /function= "approximate span of
OTHER INFORMATION: acyltransferase domain of module 6"
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  NAME/KEY:
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OTHER INFORMATION:
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LOCATION: 19149..19398
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LOCATION: 15172..16569
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LOCATION:
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OTHER INFORMATION: /function= "gene =eryA"
OTHER INFORMATION: /product= "orf3 encoding modules 5 & 6
OTHER INFORMATION: 6-deoxyerythronolide B formatio"
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LOCATION:
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14062..14610
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19492..20235
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10831..12174
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beta-ketoacylAcPsynthase domain of modul"
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beta-ketoreductase of module
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beta-ketoacylACPsynthase domain of modul"
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FILING DATE: 11-MAY 1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Casuto, Dianne
REGISTRATION NUMBER: 40,94
REFERENCE/DOCKET NUMBER: 4
                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION: TELEPHONE: 847-938-3137
                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
COMPUTER: IBM PC com
                                                                                              TOPULCE: DN MOLECULE TYPE: DN
                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
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                                                               ORIGINAL SOURCE:
                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
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                                                                                  ANTI-SENSE: NO
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STREET:
CITY: Ab
                              ORGANISM: Saccharopolyspora erythraea STRAIN: NRRL 238
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NAME/KEY:
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Abbott Laboratories D377/AP6D-2 One Abbott
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LOCATION: 10225..10483
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LOCATION: 4471..5847
OTHER INFORMATION: /function= "approximate
OTHER INFORMATION: beta-ketoacylaCPsynhase
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LOCATION: 4171..4428
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LOCATION: 97..1482
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/function= "gene eryA"
/product= "eryA ORF2 encoding modules 3 & 4 for 6-deoxyerythronolide B"
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/function= "gene =eryA"
/product= "orf3 encoding modules 5
6-deoxyerythronolide B formatio"
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module 4"
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beta-ketoacyl ACP synthase of module
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FEATURE:
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NAME/KEY:
LOCATION:
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NAME/KEY: misc_feature

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LOCATION: 18379..18921
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3831 C
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Similarity 53.0%;
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12379..13350
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14857..15114
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beta-ketoacylACPsynthase domain of modul"
                                                                                                                                                                                                                                                                                                                                                                                                                                                    /function= "approximate span of acyl carrier domain of module 6"
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beta-ketoreductase domain of module 6"
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acyltransferase domain of module
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beta-ketoacylACPsynthase domain
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acyl carrier domain of module 5"
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beta-ketoreductase of module
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module 6"
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                                                                                                                                                                                                                                                                              Score 33.8; DB 3;
Pred. No. 1.9;
0; Mismatches 82;
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                                                                                                                                                                                                                                                                                                                 Length 20235;
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RESULT 10

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us-08-676-967-5

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Best Local :
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SEQUENCE CHARACTERISTICS:
LENGTH: 2277 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
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                                                                                                                                                                                                                                            GENERAL INFORMATION:
APPLICANT: COLLINS, KATHLEEN
TITLE OF INVENTION: Human Telomerase
NUMBER OF SEQUENCES: 10
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/676,967
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TELEPHONE: (415)343-4341
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CORRESPONDENCE ADDRESS:
                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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NAME: Osman Ph.D., Richard A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: COLLINS, KATHLEEN TITLE OF INVENTION: Human Telomerase
                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
CURRENT APPLICATION DATA:
                                                                                                            COUNTRY:
ZIP: 941
               COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
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OPERATING SYSTEM: PC-DOS/MS-DOS
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CITY: San Francisco
                                                                                                                                                                                ADDRESSEE: Science & Technology Law Group STREET: 268 Bush Street, Suite 3200
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US-08-676-974-5
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Query Match
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                                                                                                                                                     TELEFAX: (415)343-4342 INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: LIBM PC compatible
COMPUTER: COMPUTER: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
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REFERENCE/DOCKET NUMBER: UCB96-055
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: OSMAN Ph.D., Richard A
REGISTRATION NUMBER: 36,627
REFERENCE/DOCKET NUMBER: UCB9
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415)343-4341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: Science & Technology Law Group
STREET: 268 Bush Street, Suite 3200
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NAME: Osman Ph.D., Richard A
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                                                                                                                                       SEQUENCE CHARACTERISTICS:
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TITLE OF INVENTION: Human Telomerase
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                                                                                STRANDEDNESS:
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CLASSIFICATION:
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                                                                   TOPOLOGY:
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                                                                                                                   LENGTH:
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DEDNESS: double
                                                                                nucleic acid
EDNESS: double
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67.1%;
10.3%;
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Score 33.2;
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 DB 2;
Length 2277;
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US-08-246-489-1
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                                                                                                                                                                                              Query Match
Best Local Similarity
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                                                                                                                                                                                  Matches
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INFORMATION FOR SEQ ID NO:
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                                                                                                                                                                                                                                                                                                        ANTI-SENSE:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: (619) 235-8550
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/901,715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/246,489
FILING DATE:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                    IMMEDIATE SOURCE:
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ATTORNEY/AGENT INFORMATION:
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APPLICANT: No. 6225049kins, Abner L
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
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OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: doub
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ZIP: 92660
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REGISTRATION NUMBER:
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                                                                                                         842 GCGACCACAGCGAGGAGGACCAGCGACCTGGAGGAGGAGCGACAGCATCGACGACGACGG 901
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                                                          AACCGTGCTGTAACTCGTGTGCGCCTGCCATGCACGAAAGGGGAATGTTTCCTGCCC 146
CGCGGCGCGGCCGCTGGGCGAGTTCATCTGCCAGCTGTGCAAGGAGGAGTACGCCGACCC
                                                                                                                                          CCTGGCCGAACACAAGCTCAAGGACGTGCGCGAGAAGATGGCCGACTTGGCGCGCATGGA 86
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                                                                                                                                                                                                                                                                                                                                                                                                          2838 base pairs
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45.3%;
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Pred. No.
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                                                                                                                                                                            Mismatches 145; Indels
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SEQ ID NO 160
; LENGTH: 1299
; TYPE: DNA
; ORGANISM: Pseudomonas aeruginosa
US-09-199-637A-160
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                                                                                                                                                                                                               Sequence 5, Application US/08173508 Patent No. 5616485
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Best Local
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APPLICANT:
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APPLICANT:
APPLICANT:
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CURRENT APPLICATION NUMBER: US/09/199,637A
CURRENT FILING DATE: 1998-11-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: 60/
PRIOR FILING DATE: 1997-11-25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: TSONGALIS, JOHN
TITLE OF INVENTION: VIRULENCE-ASSOCIATED NUCLEIC ACID
TITLE OF INVENTION: SEQUENCES AND USES THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT:
                                                 APPLICANT: Jenish, David
APPLICANT: Krieger, Timothy
TITLE OF INVENTION: STREPTOMYCES PROTEASES AND IMPROVED
TITLE OF INVENTION: STREPTOMYCES STRAINS FOR EXPRESSION
TITLE OF INVENTION: POLYPEPTIDES
                                                                                                                                          APPLICANT:
                                                                                                                                                                            APPLICANT:
                    CORRESPONDENCE ADDRESS:
                                  NUMBER OF SEQUENCES:
 ADDRESSEE:
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Mahajan-Miklos, Shalina
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 Foley & Lardner
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Pred. No. 2.1;
0; Mismatches 57;
                                                                      STRAINS FOR EXPRESSION OF PEPTIDES AND
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57;

0;

Gaps

263 944 203

Length 1299; Indels

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COUNTR: 105A
ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/173,508
FILING DATE: 23-DEC-1993
CLASSIFICATION: 435
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: BENT, Stephen A.
REGISTRATION NUMBER: 18740/125/CACO
TELECOMMUNICATION INFORMATION:
TELEPHONE: 202 672 5300
TELEFAX: 202 672 5309
TELEX: 904136
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 1777 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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Search completed: June Job time : 57 secs
                                                                                                                                                                                                                                                                                                                                                     US-08-173-508-5
                                                                                                                                                                                                                                                           Query Match 10.2%; Score 32.6; DB 1; Length 1777; Best Local Similarity 63.3%; Pred. No. 2.5; Matches 50; Conservative 0; Mismatches 29; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FEATURE:
NAME/KEY:
LOCATION:
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NAME/KNY: misc_feature
LOCATION: 190..192
OTHER INFORMATION: /note= "Met at position 1
OTHER INFORMATION: represents fmet"
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                                                                                     1599 CGTCGGCGTGGTGCTGACC 1617
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Maximum DB
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Maximum Match 100%
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and is derived by analysis of the total score distribution.
                       Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed.
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seq length: 2000000000
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Gapop 10.0 , Gapext 1.0
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321
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                                                                                                                /cgn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
/cgn2_6/ptodata/2/pubpna/US07_NEW_PUB.seq:*
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/cgn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
/cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
/cgn2_6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
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/cgn2_6/ptodata/2/pubpna/US60_PUBCOMB.seq:*
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Copyright (c) 1993 - 2003 Compugen Ltd.
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3182.538 Million cell updates/sec
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SUMMARIES

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US-10-040-739-249 US-09-796-692-4282	US-09-815-242-4163 US-09-815-242-4081	US-10-021-955-75 US-09-975-719-160	US-10-021-955-1 US-10-021-955-72	US-09-759-130B-449	US-10-042-431-79	US-09-954-456-966	US-09-954-456-700	US-10-175-523-48	US-10-044-090-167	US-10-166-087-1	US-10-166-087-17	US-09-815-242-7812	US-10-085-519-1	ID
Sequence 249, App Sequence 4282, Ap	Sequence 4163, Ap Sequence 4081, Ap	Sequence 75, Appl Sequence 160, App	Sequence 1, Appli Sequence 72, Appl	Sequence 449, App	Sequence 1143, Ap Sequence 79, Appl	Sequence 966, App	Sequence 700, App	Sequence 48, Appl	Sequence 167, App	Sequence 1, Appli	Sequence 17, Appl	Sequence 7812, Ap	Sequence 1, Appli	Description

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US-09-864-761-7033 US-09-815-242-7677 US-09-738-626-548	US-09-864-866-46 US-09-917-800A-1540 US-09-925-297-203 US-09-864-761-23764	US-09-764-864-744 US-09-729-674-157 US-10-125-237-89 US-10-105-891-89	US-09-836-821-1 US-09-861-289-1 US-10-040-739-1151 US-10-184-644-454 US-10-184-634-454	US-09-772-180A-1 US-09-815-242-4009 US-09-860-846-1 US-09-988-384B-1	US-10-040-802-4202 US-09-976-059-1 US-09-294-093B-3769 US-09-975-719-133 US-09-975-719-114
	Sequence 46, App. Sequence 1540, App. Sequence 203, App. Sequence 23764. P	Sequence 744, App Sequence 157, Appl Sequence 89, Appl Sequence 89, Appl	Sequence 1, Appli Sequence 1, Appli Sequence 1151, Ap Sequence 454, App Sequence 454, App	Sequence 1, Appli Sequence 4009, Ap Sequence 1, Appli Sequence 1, Appli	Sequence 1, Appli Sequence 3769, Ap Sequence 133, App Sequence 7, Appli Sequence 114, App

ALIGNMENTS

밁 ; TYPE: DNA ; ORGANISM: Bovine herpesvirus 2 US-10-085-519-1 RESULT 1 US-10-085-519-1 δÃ 밁 Qy 밁 Sequence 1, Application US/10085519
Patent No. US20020160018A1
GENERAL INFORMATION:
APPLICANT: Audoneet et al.
TITLE OF INVENTION: POLYNUCLEOTIDE VACCINE FORMULA, PARTICULARLY FOR TITLE OF INVENTION: TREATING BOVINE RESPIRATORY DISEASE
FILE REFERENCE: 454313-2250
CURRENT APPLICATION NUMBER: US/10/085,519
CURRENT FILING DATE: 2002-02-28
CURRENT FILING DATE: 2002-02-28 NUMBER OF SEQ ID NOS: 19 SOFTWARE: PatentIn Ver. 2 SEQ ID NO 1 LENGTH: 2799 Query Match 11.3%; Best Local Similarity 47.6%; Matches 107; Conservative PRIOR APPLICATION NUMBER: 09/232,279 PRIOR FILING DATE: 1999-01-15 2091 GGTGATCAGCACCTTTGTGGACCTAAACCTCACGGTTCTGGAGGA 2135 2031 GGACTACGTGTACTACGAGAACTACGCGTACGTGCGGCGGGTCCCGCTCGCGGAGCTGGA 2090 1971 GGGCCGCGAGCTCGTGGAGCCCTGCACCGCCAACCACAAGCGCTACTTCCGCTTTGGCGC 2030 1911 CTTCGGCAACGAGAGCGAGCCGGTGGAGGGCCAGCTCGGCGAGGACAACGAGCTGCTGCC 1970 189 GGAGGCCAGCCTGGCCGAACACACAAGCTCAAGGACGTGCGCGA 233 129 GGGGAATGTTTCCTGCCCGTTGATCGCGTCACTACAGGGATCCTCAGGCACCCACTGCGA 188 69 CGACTTGGCGCGCATGGAAACCGTGCTGTCTGAACTCGTGTGCGCCTGCCCATGCACGAAA 128 9 CTGCGAGGAGGCCAGCAGCCTGGCCGAACACAAGCTCAAGGACGTGCGCGAGAAGATGGC 68 0; Mismatches 118; Indels Score 36.2; DB 9; Length 2799; Pred. No. 0.029; 0; Gaps

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; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...
US-09-815-242-7812
US-10-166-087-17
Sequence 17, Application US/10166087
Publication No. US20030077767A1
GENERAL INFORMATION:
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CURRENT FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/191,078
PRIOR FILING DATE: 2000-03-21
PRIOR APPLICATION NUMBER: 60/206,848
PRIOR FILING DATE: 2000-05-23
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/207,727
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION NUMBER: 60/242,578
PRIOR APPLICATION UNMBER: 60/242,578
PRIOR APPLICATION UNMBER: 60/242,578
PRIOR APPLICATION UNMBER: 60/242,578
PRIOR APPLICATION UNMBER: 60/242,578
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SEQ ID NO 7812
LENGTH: 1431
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: Identification of Essential Genes
TITLE OF INVENTION: Prokaryotes
FILE REFERENCE: ELITRA.011A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Haselbeck, Robert
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: DNA
                                                                                                                                                                                                                                                            1104
                                                                                                                                                                 1164
                                                                                                                                                                                                                                                                                                                                            1044 GGGCGCGTCCATCGACAAGCAGGACCATGCCGCGAATCCGTGCGGCCAGATCGGCGAGAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: 60/269,308
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: 60/257,931
FILING DATE: 2000-12-22
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 60/253,625 FILING DATE: 2000-11-27
                                                                                                                                                                                                                                                                                                                                                                                                   135
                                                                                                                                                                                                                                                                                                                                                                                                                                                 984
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   924 GCCGTGAGCTGCGAGGCGAACCCGAAGCGCACCGCCGACATCCCGACCCTGGCGCAAAT 983
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15 GGAGGCCAGCAGCCTGGCCGAACACAAGCTCAAGGACGTGCGCGAGAAGATGGCCGACTT 74
                                                                                                                                                            CCTGGTGATCGTCACCGCCGACCACGCCCACTCCAGCCA 1202
                                                                                                                                                                                                     CATGGAAACCGTGCTGTCTGAACTCGTGTGCGCCTGCCA 293
                                                                                                                                                                                                                                                        CGTCGACCTCGACGAAGCCGTGCAGAAGGCCCTTTGCCAAGGCCGATGGCGAGAC
                                                                                                                                                                                                                                                                                                                                                                                            TGTTTCCTGCCCGTTGATCGCGTCACTACAGGGATCCTCAGGCACCCACTGCGAGGAGGC 194
                                                                                                                                                                                                                                                                                                                                                                                                                                          GACCAGCAAGGCCATCGAGCTGCTGAAGGACAATCCGAACGGCTTCTTCCTGCAGGTCGA 1043
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GGCGCGCATGGAAACCGTGCTGTCTGAACTCGTGTGCGCCTGCCATGCACGAAAGGGGAA 134
                                                                                                                                                                                                                                                                                                   CAGCAGCCTGGCCGAACACAAGCTCAAGGACGTGCGCGAGAAGATGGCCGACTTGGCGCG 254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ohlsen, Kari L.
Zyskind, Judith W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Xu, H. Howard
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Carr, Grant J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Trawick, John D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Yamamoto, Robert T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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Pred. No. 0.036;
0; Mismatches 152;
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US-10-044-090-167

Sequence 167, Application US/10044090

Patent No. US20020137081A1

; GENERAL INFORMATION:
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                                                                                          RESULT 5
                                                                                                                                                                                                                                                                                                                                                                                                                         ; ORGANISM: Streptomyces refuineus subspecies thermotolerans US-10-166-087-1
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US-10-166-087-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQ ID NO 1
LENGTH: 32539
TYPE: DNA
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Best Local Similarity
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Publication No. US20030077767A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: Genes and proteins for the biosynthesis of anthramycin FILE REFERENCE: 3014-20S
CURRENT APPLICATION NUMBER: US/10/166,087
CURRENT FILING DATE: 2002-06-11
NUMBER OF SEQ ID NOS: 51
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APPLICANT: Farnet, Chris
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CURRENT FILING DATE: 2002-06-11
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APPLICANT: Staffa, Alfredo
APPLICANT: Zazopoulos, Emmanuel
TITLE OF INVENTION: Genes and proteins for the biosynthesis of anthramycin
FILE REFERENCE: 3014-2US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: PatentIn version 3.0
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Local Similarity 58.1%;
                                                                                                                                                        11419 GATCACCGAGCTGGGGGCGCATCGACGACCCGGTGGCCGAACCCAT 11463
                                                                                                                                                                                                                                            11359 CGCCTCCAGGATCGACGGCAAGAACATCGCCGACTACGCCGCCATGGAGGTGAGCGAACT 11418
                                                                                                                                                                                 237 GATGGCCGACTTGGCGCGCGCATGGAAACCGTGCTGTCTGAACTCGT 281
                                                                                                                                                                                                                                                                                       177 CACCCACTGCGAGGAGGCCAGCAGCCTGGCCGAACACCAAGCTCAAGGACGTGCGCGAGAA 236
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Staffa, Alfredo
                                                                                                                                                                                                                                                                                                                                     Conservative
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Pred. No. 0.13;
0; Mismatches
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APPLICANT: Olga Bandman
TITLE OF INVENTION: GENES DIFFERENTIALLY EXPRESSED IN VASCULAR TISSUE ACTIVATION
FILE REFERENCE: PA-0028 US
CURRENT APPLICATION NUMBER: US/10/044,090

CURRENT FILING DATE:

2002-01-09

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; ORGANISM: Homo sapiens US-10-175-523-48
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SOFTWARE: PERL A
SEQ ID NO 167
SEQ ID NO 157
SEQ TENGTH: 3759
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 48, Application US/10175523 Publication No. US20030096264A1
                                                                                                                       NUMBER OF SEQ ID NOS: 197
SOFTWARE: PatentIn version 3.1
SEQ ID NO 48
SEQ ID NO 48
                  Query Match
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Best Local Similarity
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APPLICANT: Rajan, Prithi
TITLE OF INVENTION: MULTI-PARAMETER HIGH THROUGHPUT SCREENING ASSAYS (MPHTS)
FILE REFERENCE: 3235/1J795-US3
CURRENT APPLICATION NUMBER: US/10/175,523
CURRENT FILING DATE: 2002-06-18
CURRENT FILING DATE: 2002-06-18
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SOFTWARE: PERL Program
                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: US 60/317,828
PRIOR FILING DATE: 2001-09-07
PRIOR APPLICATION NUMBER: US 60/325,150
PRIOR FILING DATE: 2001-09-25
                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: US 60/299,151 PRIOR FILING DATE: 2001-06-18
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                                                                                                                                                                                 PRIOR FILING DATE:
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ORGANISM: Homo sapiens
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OTHER INFORMATION: Inc
                                                                                          TYPE: DNA
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                                                                                                         LENGTH:
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                                                                                                                                                                                             APPLICATION NUMBER: US 60/333,047
FILLING DATE: 2001-11-14
APPLICATION NUMBER: US 60/349,936
FILING DATE: 2002-01-18
APPLICATION NUMBER: US 60/361,834
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     134 ATGTTTCCTGCCCGTTGATCGCGTCACTACAGGGATCCTCAGGCACCCACTGCGAGGAGG 193
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TGGCGCGCATGGAAACCGTGCTGTCTGAACTCGTGTGCGCCTGCCATGCACGAAAGGGGA 307
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CCCTCATCCTGGGCTTCATGGCCGGCTCCCGAGAGAACCCCGTGCCAGGAGCAGGTGGACG
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Hook, Derek
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53.0%;
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Pred. No. 0.24
0; Mismatches
Score 33;
Pred. No.
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DB 9;
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                 Length 2838;
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Best Local Similarity 45.3%;
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PRIOR APPLICATION NUMBER: US/60/233,617
PRIOR FILING DATE: 2000-09-18
PRIOR BODITANTO: .....
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PRIOR FILING DATE: 2000-09-25
PRIOR APPLICATION NUMBER: US/60/235,637
PRIOR FILING DATE: 2000-09-26
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PRIOR APPLICATION NUMBER: US/60/234,923
PRIOR FILING DATE: 2000-09-25
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CURRENT FILING DATE: 2001-09-18
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APPLICATION NUMBER: US/60/235,720
FILING DATE: 2000-09-27
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Pred. No. 0.
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US-09-954-456-966
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LENGTH: 2838
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Best Local
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TYPE: DNA
ORGANISM: Homo sapiens
-09-954-456-966
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CURRENT FILING DATE: 2001-09-18
PRIOR APPLICATION NUMBER: US/60/233,617
PRIOR FILING DATE: 2000-09-18
PRIOR APPLICATION NUMBER: US/60/234,052
PRIOR FILING DATE: 2000-09-20
PRIOR FILING DATE: 2000-09-25
PRIOR FILING DATE: 2000-09-25
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NUMBER OF SEQ ID NOS: 2276
SOFTWARE: Patentin version
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TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using Canc
TITLE OF INVENTION: Sets
FILE REFERENCE: 689290-76
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APPLICATION NUMBER: US/60/235,840
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                    1044 GTGCGCCAAGGTCTTCAGCTGCCCGGCCAACCTGGCCTCGCCACCGCCGCTGGCACAAACC 1103
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Pred. No. 0.31;
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US-10-042-431-79
; Sequence 79, Application US/10042431
; Publication No. US20020182675A1
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LENGTH: 2838
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; ORGANISM: Homo sapiens
US-09-954-456-1143
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US-09-954-456-1143
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SOFTWARE: PatentIn ver
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PRIOR APPLICATION NUMBER: US/60/235,720
PRIOR FILING DATE: 2000-09-27
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CURRENT FILING DATE: 2001-09-18
PRIOR APPLICATION NUMBER: US/60/233,617
PRIOR FILING DATE: 2000-09-18
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Local Similarity 45.3%;
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1104 GCGGCCGCGCCGCCGCCGCC 1128
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2000-09-27
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Pred. No. 0.31;
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; LENGTH: 4308
; TYPE: DNA
; ORGANISM: Bos sp.
US-10-042-431-79
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CURRENT APPLICATION NUMBER: US/10/042,431

CURRENT FILING DATE: 2001-10-25

PRIOR APPLICATION NUMBER: US 09/333,159

PRIOR FILING DATE: 1999-06-14

PRIOR APPLICATION NUMBER: US 09/578,063

PRIOR FILING DATE: 2000-05-24

NUMBER OF SEQ ID NOS: 79
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 449, Application US/09759130B Publication No. US20030022279A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Millennium Pharmaceuticals, Inc.
APPLICANT: McCarthy, Sean A
APPLICANT: Fraser, Christopher C
APPLICANT: Sharp, John D
APPLICANT: Barnes, Thomas S
APPLICANT: Kirst, Susan J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING DIAGNOSTIC, TITLE OF INVENTION: PREVENTIVE, THERAPEUTIC, AND OTHER USES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: BARNES, Thomas M
APPLICANT: FRASER, Christopher C
APPLICANT: SHARP, John D
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: MCCARTHY, APPLICANT: BARNES, '
                                                                                                                                                                                                                                                                                                APPLICANT: Holtzman, Douglas A
TITLE OF INVENTION: NOVEL GENES ENCODING PROTEINS HAVING
TITLE OF INVENTION: PROGNOSTIC, DIAGNOSTIC, PREVENTIVE, THERAPEUTIC, AND OTHER
TITLE OF INVENTION: USES.
FILE REFERENCE: MPI00-5350MNIM
                                                                                                          PRIOR APPLICATION NUMBER: US 09/559,497
PRIOR FILING DATE: 2000-04-27
PRIOR APPLICATION NUMBER: US 09/578,063
PRIOR FILING DATE: 2000-05-24
                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: US 09/479,249 PRIOR FILING DATE: 2000-01-07
                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/759,130B CURRENT FILING DATE: 2002-09-16
                                           PRIOR
                                                                 PRIOR
                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT:
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                                      APPLICATION NUMBER: US 09/333,159 FILING DATE: 1999-06-14 APPLICATION NUMBER: US 09/596,194
APPLICATION NUMBER: US 09/342,364
                     FILING DATE: 2000-07-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3535 GTGTGCGATGACTCCTGGAGCCTGGCAG-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        121 GCACGAAAGGGGAATGTTTCCTGCCCGTTGATCGCGTCACTACAGGGATCCTCAGGCACC
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Barnes, Thomas S
Kirst, Susan J
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mackay, Charles R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Leiby, Kevin R
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; LENGTH: 5502
; TYPE: DNA
; ORGANISM: human
US-10-021-955-1
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US-10-021-955-1
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RESULT 13
US-10-021-955-72
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PRIOR APPLICATION NUMBER: US 09/608,452
PRIOR FILING DATE: 2000-06-30
PRIOR APPLICATION NUMBER: US 09/393,996
PRIOR FILING DATE: 1999-09-10
PRIOR APPLICATION NUMBER: US 09/602,871
PRIOR APPLICATION NUMBER: US 09/602,871
PRIOR APPLICATION NUMBER: US 09/420,707
PRIOR FILING DATE: 1999-10-19
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SEQ ID NO 449
LENGTH: 4308
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Best Local Similarity
Matches 94; Conserv
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APPLICANT: Boerkoel, Cornelius F
APPLICANT: Takashima, Hiroshi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: US 60/255,217 PRIOR FILING DATE: 2000-12-13 NUMBER OF SEQ ID NOS: 93
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/10/021,955
CURRENT FILING DATE: 2001-12-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: Takashima, Hiroshi
TITLE OF INVENTION: Defects in Periaxin Associated with Myelinopathies
FILE REFERENCE: P02086USi/10026309
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM: Bovine
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                                                                                                                                                                                                                                                                                      Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3475 GGAGGAGACAGCGAGTGCTCAGGGCGGGTGGAGGTGTGGCACAACGGCTCCTGGGGCACC
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                                                                                                                                                                            593 GCCCGGGACCGTGTCTGGCTACGAGATCAAGGGCCCGCGGGCCAAGGTGGCCAAGCTGGT 652
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                                                                                      653 ACGCGTGCTTAGCCCGGCCCCGGCCCTGGACTGCCCCAGCGATCC 697
                                                                                                                                 78 GCGCATGGAAACCGTGCTGTCTGAACTCGTGTGCGCCTGCCATGC 122
                                                                                                                                                                                                                    18 GGCCAGCAGCCTGGCCGAACACAAGCTCAAGGACGTGCGCGAGAAGATGGCCGACTTGGC
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53.7%;
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57.1%;
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Pred. No. 0.34;
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                                                                                                                                                                                                                                                                                                          DB 9; Length 5502;
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Sequence 72, Application US/100 Publication No. US20030039987A1

Application US/10021955

GENERAL INFORMATION:

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RESULT 15
US-09-975-719-160
IS-09-975-719-160
Sequence 160, Application US/09975719
Publication No. US20030022349A1
GENERAL INFORMATION:
APPLICANT: Ausubel, Frederick M.
APPLICANT: Rahme, Laurence G.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; TYPE: DNA
; ORGANISM: Human
US-10-021-955-75
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; Sequence 75, Application US/10021955

; Publication No. US20030039987A1
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; ORGANISM: Human
US-10-021-955-72
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APPLICANT: Lupski, James R

APPLICANT: Lupski, Cornelius F

APPLICANT: Beerkeel, Cornelius F

APPLICANT: Takashima, Hiroshi

TITLE OF INVENTION: Defects in Periaxin Associated with Myelinopathies

FILE REFERENCE: P02086US1/10026309

CURRENT APPLICATION NUMBER: US/10/021,955

CURRENT FILING DATE: 2001-12-13

PRIOR FILING DATE: 2006-12-13

PRIOR FILING DATE: 2006-12-13

NUMBER OF SEQ ID NOS: 93

SOFTWARE: Patentin version 3.1
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Best Local Similarity
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LENGTH: 5502
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SEQ ID NO 7
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APPLICANT: Lupski, James R
APPLICANT: Boerkoel, Cornelius F
APPLICANT: Takashima, Hiroshi
TITLE OF INVENTION: Defects in Periaxin Associated with Myelinopathies
FILE REFERENCE: P02086USi/10026309
CURRENT APPLICATION NUMBER: US/10/021,955
CURRENT FILING DATE: 2001-12-13
CURRENT FILING DATE: 2001-12-13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 5502
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Local Similarity 57.1%;
nes 60; Conservative
                                                                                                                                                                                                          653 ACGCGTGCTTAGCCCGGCCCCGGCCCTGGACTGCCCCAGCGATCC 697
                                                                                                                                                                                                                                                                                               593 GCCCGGGACCGTGTCTGGCTACGAGATCAAGGGCCCGCGGGCCAAGGTGGCCAAGCTGGT 652
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                                                                                                                                                                                                                                                   78 GCGCATGGAAACCGTGCTGTCTGAACTCGTGTGCGCCTGCCATGC 122
                                                                                                                                                                                                                                                                                                                                            18 GGCCAGCAGCCTGGCCGAACACAAGCTCAAGGACGTGCGCGAGAAGATGGCCGACTTGGC 77
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Pred. No. 0.34;
0; Mismatches 4
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; TITLE OF INVENTION: VIRULENCE-ASSOCIATED NUCLEIC ACID
; TITLE OF INVENTION: SEQUENCES AND USES THEREOF
; FILE REFERENCE: 00786/361003
; CURRENT APPLICATION NUMBER: US/09/975,719
; CURRENT FILING DATE: 2001-10-10
; PRIOR APPLICATION NUMBER: US 09/199,637
; PRIOR FILING DATE: 1998-11-25
; PRIOR APPLICATION NUMBER: US 60/066,517
; PRIOR APPLICATION NUMBER: US 60/066,517
; PRIOR FILING DATE: 1997-11-25
; NUMBER OF SEQ ID NOS: 437
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO 160
; LENGTH: 1299
Search completed: June Job time: 138 secs
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Best Local S
Matches 67
                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: DNA
                                                                                                                                                                                                                                                                                                                  Local Similarity es 67; Conserv
                                                                               1005 CCTG 1008
                                                                                                                  264 CGTG 267
                                                                                                                                                        945 GGACGACGACAAGATCAAGCGCAACCGCGAATTCATGAACGTCTTCCAGCAATTGCGCGC 1004
                                                                                                                                                                                                                                   885 CCTCTTCCCCGGGTATCCCGAGGGTTACTACGAGAACCACTTCCTGCATTCCTTCGAGCT
                                                                                                                                                                                                                                                              204 GCCCGAACACCAAGCTCAAGGACGTGCGCGAGAAGATGGCCGACTTGGCGCGCATGGAAAC 263
                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                   10.2%;
                2003, 07:36:45
                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                                                                                                            Score 32.8; DB Pred. No. 0.33; 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                      DB 9;
                                                                                                                                                                                                                                                                                                                57;
                                                                                                                                                                                                                                                                                                                                                      Length 1299;
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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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Perfect score:
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1: \SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1980.DAT: *
2: \SIDS2/gcgdata/geneseq/geneseqp-emb1/AA1981.DAT: *
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Listing first 45 summaries
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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snigeria ilexneri	Chi-11-61-Chambany	Synthetic cadmium/	Synthetic cadmium/	Synthetic cadmium/	Synthetic cadmium/	Carried Continually	Synthetic cadmium/	Synthetic cadmium/	Shirtnerto camilimity	nunthotic codming.	Synthetic cadmium/	Synthetic Merk Che		Description			

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	HTRM clone 2674047	Human protein SEQ	Human protein SEQ	Drosophila melanog	Novel human diagno	Murine Wnt-3a prot	Novel human diagno	Human cytoskeletal	Drosophila melanog	Novel human diagno	ria mo	zinc f	human	human	human				~		occcus p	protein	e pro	cell	11			e pro		ococcus e	product	product	in prod	MerR protein which
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ALIGNMENTS

RESULT 1

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AAU97552
ID AAU97552 standard; Protein; 117 AA.

XX
AC AAU97552;
XX
DT 13-AUG-2002 (first entry)
XX
Synthetic Merk chelon variant.

XW
Mercuric ion; contaminated soil; ground water; hydroponic solution;
KW irrigation water; waste stream; contaminated aqueous medium;
KW biological fluid; gastrointestinal tract; chelon protein;
KW enteric bacteria; toxic metal ion; mercury; cadmium; divalent cation;
XX
enteric bacteria; toxic metal ion; mercury; cadmium; divalent cation;
XX
Neavy metal binding protein; Merk.

XX
PN
W0200230962-A2.
XX
PP
12-OCT-2000; 2000WS-240465P.
XX
PF
12-OCT-2000; 2000WS-240465P.
XX
12-OCT-2000; 2000WS-240465P.
XX
XX
PF
Summers AO, Caguiat JJ;
XX
WPI; 2002-435437/46.
DR
N-PSDB; ABK52207, ABK52213.
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CC producing a protein in a host-cell, by infecting or transforming a host cell capable of expressing a chelon coding sequence with a vector CC comprising a protein in a host-cell, by infecting or transforming a host cell capable of expressing a chelon coding sequence with a vector CC creyion for the protein to produce a recombinant host cell and culturing CC The nucleic acid encoding the chelon protein is useful for binding CC divalent mercuric ions, to take up, sequester and concentrate the heavy CC irrigation water of waste streams. The DNA of the invention, when CC inmobilised onto a solid support, is useful for concentrating heavy metal cons from contaminated soil, ground water, hydroponic solutions or constantiant environment waste streams or contaminated concentrating heavy metal considerabilised onto a solid support, is useful for concentrating heavy metal considerabilised onto a solid support, is useful for concentrating heavy metal considerabilised onto a solid support, is useful for concentrating heavy metal concentration and concentration and concentration are also useful in water treatment resins. The molecules of the invention are also useful in water treatment resins. The nucleic acid of the invention is highly specific and binds divalent cation such as mercury or cadmium with high affinity. The present amino concentration contaminated concentration of the heavy metal binding proteins of the invention.

Note: ABK52207 encodes only amino acids 1-107 of this protein.
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention relates to a new non-naturally occurring
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                                                                                                                                                                                                                                                                    Mercuric ion; contaminated soil; ground water; hydroponic solution; irrigation water; waste stream; contaminated aqueous medium; biological fluid; gastrointestinal tract; chelon protein; enteric bacteria; toxic metal ion; mercury; cadmium; divalent catio;
                                                                                                                                                                                                                                                                                                                                                                                                Synthetic cadmium/mercury ion binding chelon protein #8
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAU97560 standard; Protein; 117
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                                              12-OCT-2001; 2001WO-US31819.
                                                                                                                                                WO200230962-A2
                                                                                                                                                                                            Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                 13-AUG-2002
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12-OCT-2000; 2000US-240465P.
                                                                                               18-APR-2002
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                                                                                                                                                                                                                                               metal binding
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     117 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first entry)
                                                                                                                                                                                                                                               protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             100.0%;
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RESULT 3
AAU97553
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cc which binds mercuric ions. The invention is useful for recombinant of expressing a chelon coding sequence with a vector cell capable of expressing a chelon coding sequence with a vector comprising a promoter active in the host cell operably linked to a coding cregion for the protein to produce a recombinant host cell and culturing client recombinant host cell under conditions, where DNA is expressed.

CC The nucleic acid encoding the chelon protein is useful for binding coding creatal ions from contaminated soil, ground water, hydroponic solutions or irrigation water of waste streams. The DNA of the invention, when criminated environment waste streams or concentrate the heavy considered from contaminated environment waste streams or concentrating heavy metal constrongent of the invention and celimination of mercuric ion from gastrointestinal tracts of animals or elimination of mercuric ion from gastrointestinal tracts of animals or chumans exposed to toxic metal ions such as mercury and/or cadmium. The nucleic acid of the invention are also useful in water treatment resins. The nucleic acid of the invention is highly specific and binds divalent cation such as mercury or cadmium with high affinity. The present amino confinition cadmium/mercury ion binding chelon proteins of the invention. This sequence is one of the heavy metal binding proteins termed chelons.
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                recombinant DNA molecule comprising a sequence encoding a chelon protein which binds mercuric ions. The invention is useful for recombinantly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention relates to a new non-naturally occurring
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 4; Page 22; 42pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (UYGE-) UNIV GEORGIA RES FOUND INC.
                                                                              Mercuric ion; contaminated soil; ground water; hydroponic solution; irrigation water; waste stream; contaminated aqueous medium; biological fluid; gastrointestinal tract; chelon protein; enteric bacteria; toxic metal ion; mercury; cadmium; divalent cation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        of the invention.
                                                                                                                                                                                        Synthetic cadmium/mercury ion binding chelon protein #1
                                                                                                                                                                                                                                     13-AUG-2002 (first entry)
                                                                                                                                                                                                                                                                                                                          AAU97553 standard; Protein; 117 AA.
                                                            heavy metal binding protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                    61
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99.1%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length 117;
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WO200230962-A2

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the recombinant host cell under conditions, where DNA is expressed.

CC The nucleic acid encoding the chelon protein is useful for binding

CC divalent mercuric ions, to take up, sequester and concentrate the heavy

CC metal ions from contaminated soil, ground water, hydroponic solutions or

CC immobilised onto a solid support, is useful for concentrating heavy metal

CC ions from contaminated environment waste streams or contaminated

CC aqueous medium including biological fluids. The nucleic acid, when

CC recombinantly expressed in enteric bacteria (which are nontoxigenic and

CC nonpathogenic), is suitable for use in the in vivo sequestration and

CC elimination of mercuric ion from gastrointestinal tracts of animals or

CC humans exposed to toxic metal ions such as mercury and/or cadmium. The

CC molecules of the invention are also useful in water treatment resins.

CC The nucleic acid of the invention is highly specific and binds divalent

CC cation such as mercury or cadmium with high affinity. The present amino

CC acid sequence represents one of a collection (AAU97550 AU97560) of

CC This sequence is one of the heavy metal binding proteins termed chelons
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 115;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Mercuric ion; contaminated soil; ground water; hydroponic solution;
                                               Synthetic cadmium/mercury ion binding chelon protein #4.
                                                                                                                                                                          AAU97556 standard; Protein;
                                                                                              13-AUG-2002
                                                                                                                                      AAU97556;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           producing a protein in a host-cell, by infecting or transforming a host cell capable of expressing a chelon coding sequence with a vector comprising a promoter active in the host cell operably linked to a coding region for the protein to produce a recombinant host cell and culturing the recombinant host cell under conditions, where DNA is expressed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention relates to a new non-naturally occurring recombinant DNA molecule comprising a sequence encoding a chelon protein which binds mercuric ions. The invention is useful for recombinantly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 4; Page 22; 42pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Novel non-naturally occurring recombinant DNA molecule encoding a chelon protein useful for binding divalent cation mercury from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                contaminated soil, water, aqueous medium including biological fluids -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (UYGE-) UNIV GEORGIA RES FOUND INC.
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                                                                                                                                                                                                                                                                                   61 HCEEVSSLAEHKLKDVREKMADLARMETVLSELVCACHARKGNVSCPSAWSHPQFEK 117
                                                                                                                                                                                                                                                                                                                            61 HCEEASSLAEHKLKDVREKMADLARMETVLSELVCACHARKGNVSCPSAWSHPQFEK 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                            1 MTHCEEASSLAEHKLKDVREKMADLARMETVLSELVCACHARKGNVSCPLIASLQGSSGT 60
                                                                                                                                                                                                                                                                                                                                                                      MTHCEEVSSLAEHKLKDVREKMADLARMETVLSELVCACHARKGNVSCPLIASLQGSSGT 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   117 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Caguiat JJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  98.7%;
98.3%;
                                                                                                                                                                                 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 605; DB 23
Pred. No. 2e-52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DB 23; Length 117;
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AAU97557 ID AAU9 XX

AAU97557 standard; Protein; 117 AA

RESULT

Дb Q 밁 Ş

61

61 HCEEASSLAEHKLKDVREKMADLARMETVLSELVCACHARKGNVSCPSAWSHPQFEK 117

HCEEASSLAEHKLKDVREQMADLARMETVLSELVCACHARKGNVSCPSAWSHPQFEK 117

1 MTHCEEASSLAEHKLKDVREKMADLARMETVLSELVCACHARKGNVSCPLIASLQGSSGT

MTHCEEASSLAEHKLKDVREQMADLARMETVLSELVCACHARKGNVSCPLIASLQGSSGT

60

Matches 115; Query Match Best

Conservative

Local Similarity

98.7**%**; 98.3**%**;

Score 605; DB 2 Pred. No. 2e-52; Mismatches

DB 23; 0;

Length 117; Indels

0;

Gaps

0;

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ions from contaminated environment waste streams or contaminated aqueous medium including biological fluids. The nucleic acid, when recombinantly expressed in enteric bacteria (which are nontoxigenic and nonpathogenic), is suitable for use in the in vivo sequestration and elimination of mercuric ion from gastrointestinal tracts of animals or humans exposed to toxic metal ions such as mercury and/or cadmium. The molecules of the invention are also useful in water treatment resins. The nucleic acid of the invention is highly specific and binds divalent cation such as mercury or cadmium with high affinity. The present amino acid sequence represents one of a collection (AMU97553-AMU97560) of synthetic cadmium/mercury ion binding chelon proteins of the invention. This sequence is one of the heavy metal binding proteins termed chelons of the invention.
Sequence
                                                                                                                                                                                                                                                                                                                                                        The nucleic acid encoding the chelon protein is useful for binding divalent mercuric ions, to take up, sequester and concentrate the heavy metal ions from contaminated soil, ground water, hydroponic solutions or irrigation water of waste streams. The DNA of the invention, when immobilised onto a solid support, is useful for concentrating heavy metal tons from contaminated outliness the stream of the invention of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            cell capable of expressing a chelon coding sequence with a vector comprising a promoter active in the host cell operably linked to a coding region for the protein to produce a recombinant host cell and culturing the recombinant host cell under conditions, where DNA is expressed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel non-naturally occurring recombinant DNA molecule encoding a chelon protein useful for binding divalent cation mercury from contaminated soil, water, aqueous medium including biological fluids
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biological fluid; gastrointestinal tract; chelon protein;
enteric bacteria; toxic metal ion; mercury; cadmium; divalent cation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            producing a protein in a host-cell, by infecting or transforming a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        which binds mercuric ions.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 recombinant
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                                                invention.
117 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DNA molecule comprising a sequence encoding a chelon protein mercuric ions. The invention is useful for recombinantly
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AAU97557;

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                                                                                                                                                                                                                                                                                                                       CC recombinant DNA molecule comprising a sequence encoding a chelon protein comprising a sequence encoding a chelon protein combinant binds mercuric ions. The invention is useful for recombinantly countries of expressing a chelon coding sequence with a vector cell capable of expressing a chelon coding sequence with a vector comprising a promoter active in the host cell operably linked to a coding region for the protein to produce a recombinant host cell under conditions, where DNA is expressed. CC The nucleic acid encoding the chelon protein is useful for binding cometal ions from contaminated soil, ground water, hydroponic solutions or irrigation water of waste streams. The DNA of the invention, when claim from contaminated environment waste streams or contaminated environment waste streams or contaminated contaminated environment environmen
                                                                                                                                                                  Matches
                                                                                                                                                                                                              Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel non-naturally occurring recombinant DNA molecule encoding a chelon protein useful for binding divalent cation mercury from contaminated soil, water, aqueous medium including biological fluids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               13-AUG-2002
                                                                                                                                                                                                                                                              Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 4; Page 22; 42pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2002-435437/46.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    heavy metal binding protein.
                      61
                                                                                                                                                                                          Local
                                                                                            MTHCEEASSLAEHKLKDVREKMADLARMETVLSELVCACHARKGNVSCPLIASLQGSSGT 60
                      HCEEASSLAEHKLKDVREKMADLARMETVLSELVCACHARKGNVSCPSAWSHPQFEK 117
                                                                   MTHCEEASSLAEHKLKDVREKMADLARVETVLSELVCACHARKGNVSCPLIASLQGSSGT 60
invention.
                                                                                                                                                                                          Similarity
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                                                                                                                                                                                                                                                                117
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                                                                                                                                                               Conservative
                                                                                                                                                                                        98.7%;
98.3%;
                                                                                                                                                                  2
                                                                                                                                                                                     Score 605; DB 2
Pred. No. 2e-52;
                                                                                                                                                                    Mismatches
                                                                                                                                                                                                              DB 23;
                                                                                                                                                                  0;
                                                                                                                                                                                                              Length 117;
                                                                                                                                                                    Indels
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0

Matches 115; Conserv

Conservative

2;

98.7%; 98.3%;

Score 605; Db 2-4 No. 2e-52; Mismatches

DB 23;

Length 117;

0

Gaps

0

Query Match

Sequence

117 AA

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                                                                                     Comprising a protein in elaces to a new non-naturally occurring combinant DNA molecule comprising a sequence encoding a chelon protein components are the protein in a host-cell, by infecting or transforming a host cell capable of expressing a chelon coding sequence with a vector comprising a protein to produce a recombinant host cell under conditions, where DNA is expressed. CC The nucleic acid encoding the chelon protein is useful for binding contaminated soil, ground water, hydroponic solutions or irrigation water of waste streams. The DNA of the invention, when capably advantaged in enteric bacteria (which are nontoxigenic and concentrating the combinant host cell under conditions, where DNA is expressed. CC immobilised onto a solid support, is useful for concentrating heavy metal ions from contaminated environment waste streams or contaminated consumment in enteric bacteria (which are nontoxigenic and compathogenic), is suitable for use in the in vivo sequestration and compathogenic), is suitable for use in the in vivo sequestration and compathogenic), is suitable for use in the in vivo sequestration and compathogenic), is suitable for use in the in vivo sequestration and compathogenic), is suitable for use in the in vivo sequestration and compathogenic), is suitable for use in the in vivo sequestration and compathogenic), is suitable for use in the in vivo sequestration and compathogenic), is suitable for use in the in vivo sequestration and compathogenic), is suitable for use in the in vivo sequestration and compathogenic acid of the invention are also useful in water treatment resins.

CC This sequence represents one of a collection (AAU97553-AAU97560) of synthetic cadmium/mercury ion binding chelon proteins of the invention.

CC synthetic cadmium/mercury ion binding chelon proteins of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           irrigation water; waste stream; contaminated aqueous medium; biological fluid; gastrointestinal tract; chelon protein; enteric bacteria; toxic metal ion; mercury; cadmium; divalen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic cadmium/mercury ion binding chelon protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel non-naturally occurring recombinant DNA molecule encoding a chelon protein useful for binding divalent cation mercury from contaminated soil, water, aqueous medium including biological fluids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 4; Page 22; 42pp; English.
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                                                      of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention relates to a new non-naturally occurring
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                                                                           This sequence is one of the heavy metal binding proteins termed chelons
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conviction to the intercept comprising a sequence encoding a chelon protein consisting a protein in a host-cell, by infecting or transforming a host cell capable of expressing a chelon coding sequence with a vector cell capable of expressing a chelon coding sequence with a vector comprising a promoter active in the host cell operably linked to a coding the recombinant host cell under conditions, where DNA is expressed. Cregion for the protein to produce a recombinant host cell and culturing created in the chelon protein is useful for binding created ions from contaminated soil, ground water and concentrate the heavy created ions from contaminated soil, ground water, hydroponic solutions or immobilised onto a solid support, is useful for concentrating heavy metal constrainment waste streams or contaminated creations from contaminated environment waste streams or contaminated crecombinantly expressed in enteric bacteria (which are nontoxigenic and conpathogenic), is suitable for use in the in vivo sequestration and crecombinantly expressed in enteric bacteria (which are nontoxigenic and conpathogenic), is suitable for use in the invivo sequestration and chimans exposed to toxic metal ions such as mercury and/or cadmium. The nucleus of the invention are also useful in water treatment resins. The nucleus acid of the invention are also useful in water treatment resins. The nucleus acid of the invention are also useful in specific and binds divalent cation such as mercury or cadmium with high affinity. The present amino acid sequence represents one of a collection (AAU97553-AAU97560) of synthetic cadmium/mercury ion binding chelon proteins of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  chelon protein useful for binding divalent cation mercury from contaminated soil, water, aqueous medium including biological fluids -
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CC producing a protein in a host-cell, by infecting or transforming a host cell capable of expressing a chelon coding sequence with a vector cc comprising a promoter active in the host cell operably linked to a coding region for the protein to produce a recombinant host cell and culturing the recombinant host cell under conditions, where DNA is expressed.

CC The nucleic acid encoding the chelon protein is useful for binding cc divalent mercuric ions, to take up, sequester and concentrate the heavy metal ions from contaminated soil, ground water, hydroponic solutions or cirrigation water of waste streams. The DNA of the invention, when cc inmobilised onto a solid support, is useful for concentrating heavy metal ions from contaminated environment waste streams or contaminated colding biological fluids. The nucleic acid, when crecombinantly expressed in enteric bacteria (which are nontoxigenic and nonpathogenic), is suitable for use in the in vivo sequestration and compathogenic), is suitable for use in the in vivo sequestration and compathogenic).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
nonpathogenic), is suitable for use in the in vivo seques elimination of mercuric ion from gastrointestinal tracts
                                                                                                                                                                                                                                                                                                                                                                         Claim 4; Page 22; 42pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                       Novel non-naturally occurring recombinant DNA molecule encoding a chelon protein useful for binding divalent cation mercury from contaminated soil, water, aqueous medium including biological fluids
                                                                                                                                                                                                                                                                                                which binds mercuric ions.
                                                                                                                                                                                                                                                                                                                                  The present invention relates to a new non-naturally occurring
                                                                                                                                                                                                                                                                                                                        recombinant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Summers AO,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12-OCT-2000; 2000US-240465P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12-OCT-2001; 2001WO-US31819
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18-APR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  irrigation water; waste stream; contaminated aqueous medium; biological fluid; gastrointestinal tract; chelon protein; enteric bacteria; toxic metal ion; mercury; cadmium; divalent cation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mercuric ion; contaminated soil; ground water; hydroponic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Synthetic cadmium/mercury ion binding chelon protein #3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAU97555 standard; Protein; 117 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (UYGE-) UNIV GEORGIA RES FOUND INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200230962-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  heavy metal binding protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2002-435437/46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MTHCEEASSLAEHKLKDVREKMADLARMETVLSELVCACHARKGNVPCPLIASLQGSSGT 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Similarity
                                                                                                                                                                                                                                                                                                            DNA molecule comprising a sequence encoding a chelon protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     117 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Caguiat JJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98.4%;
                                                                                                                                                                                                                                                                                              The invention is useful for recombinantly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 603; DB 23; Pred. No. 3.1e-52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 117;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               solution;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps
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Matches
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The present invention relates to a new non-naturally occurring recombinant DNA molecule comprising a sequence encoding a chelon protein which binds mercuric ions. The invention is useful for recombinantly producing a protein in a host-cell, by infecting or transforming a host cell capable of expressing a chelon coding sequence with a vector comprising a promoter active in the host cell operably linked to a coding region for the protein to produce a recombinant host cell and culturing the recombinant host cell under conditions, where DNA is expressed. The nucleic acid encoding the chelon protein is useful for binding divalent mercuric ions, to take up, sequester and concentrate the heavy metal ions from contaminated soil, ground water, hydroponic solutions or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    irrigation water; waste stream; contaminated aqueous medium; biological fluid; gastrointestinal tract; chelon protein; enteric bacteria; toxic metal ion; mercury; cadmium; divalent cation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Synthetic cadmium/mercury ion binding chelon protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAU97554 standard; Protein; 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                contaminated soil, water, aqueous
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel non-naturally occurring recombinant DNA molecule encoding a chelon protein useful for binding divalent cation mercury from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2002-435437/46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Summers AO,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12-OCT-2001; 2001WO-US31819
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              heavy metal binding protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mercuric ion; contaminated soil; ground water; hydroponic solution;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       13-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAU97554;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (UYGE-) UNIV GEORGIA RES FOUND INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12-OCT-2000; 2000US-240465P
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               vocar
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            115;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                           Page 22; 42pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  117 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Caguiat JJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             98.0%;
98.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                medium including biological fluids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
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ions from contaminated environment waste streams or contaminated aqueous medium including biological fluids. The nucleic acid, when recombinantly expressed in enteric bacteria (which are nontoxigenic and nonpathogenic), is suitable for use in the in vivo sequestration and elimination of mercuric ion from gastrointestinal tracts of animals or humans exposed to toxic metal ions such as mercury and/or cadmium. The molecules of the invention are also useful in water treatment resins. The nucleic acid of the invention is highly specific and binds divalent cation such as mercury or cadmium with high affinity. The present amino acid sequence represents one of a collection (AAU97563) of synthetic cadmium/mercury ion binding chelon proteins of the invention. This sequence is one of the heavy metal binding proteins termed chelons of the invention.
                                                                 of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                              irrigation water of waste streams. The DNA of the invention, when immobilised onto a solid support, is useful for concentrating heavy metal
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Sequence

118 AA;

DB 23;

Length 118;

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                                                                 믕
                                                                                                                                                                    Matches
                                                                                                                                                                                  Query Match
Best Local
AAU97551 standard; Protein; 144 AA
                                                               61 THCEEASSLVEHKLKDVREKMADLARMETVLSELVCACHARKGNVSCPSAWSHPQFEK 118
                                                                             60 THCEEASSLAEHKLKDVREKMADLARMETVLSELVCACHARKGNVSCPSAWSHPQFEK 117
                                                                                                                               1 MTHCBEASSLAEHKLKDVREK-MADLARMETVLSELVCACHARKGNVSCPLIASLQGSSG
                                                                                                                 115;
                                                                                                                                                                                  Similarity
                                                                                                                                                                      Conservative
                                                                                                                                                                                  97.0%;
97.5%;
                                                                                                                                                                                  Score 594.5;
Pred. No. 2.7
                                                                                                                                                                       Mismatches
                                                                                                                                                                                  .2e-51;
                                                                                                                                                                         Indels
                                                                                                                                                                          <u>,</u>
                                                                                                                                                                         Gaps
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RESULT 10
AAU97551
ID AAU97757
XX AAU97
AC AAU97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            irrigation water;
biological fluid;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Shigella flexneri wild-type MerR protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13-AUG-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           heavy metal binding protein; MerR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mercuric ion; contaminated soil; ground water; hydroponic solution;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           bacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 waste stream; contaminated aqueous medium;
gastrointestinal tract; chelon protein;
toxic metal ion; mercury; cadmium; divalent cation;
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Shigella flexneri.

WO200230962-A2

12-OCT-2001; 2001WO-US31819

12-OCT-2000; 2000US-240465P

(UYGE-) UNIV GEORGIA RES FOUND INC

Summers AO, Caguiat JJ;

N-PSDB; ABK52206. WPI; 2002-435437/46.

Novel non-naturally occurring recombinant DNA molecule encoding a chelon protein useful for binding divalent cation mercury from contaminated soil, water, aqueous medium including biological fluids

Disclosure; Page 20; 42pp; English

The present invention relates to a new non-naturally occurring which binds DNA molecule comprising a sequence encoding a chelon protein mercuric ions. The invention is useful for recombinantly

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RESULT 11
AAAYO1816
ID AAYO1816
ID AAYO1816
AC AAAYO1
AC AAAYO1
AC AAAYO1
AC AAAYO1
AC AAAYO1
XX Heavy
KW Heavy
KW Capac
KW Zinc;
KW Capac
KW Food.
XX Pseud
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       В
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CC producing a protein in a host-cell, by infecting or transforming a host cell capable of expressing a chelon coding sequence with a vector comprising a promoter active in the host cell operably linked to a coding region for the protein to produce a recombinant host cell and culturing the recombinant host cell under conditions, where DNA is expressed. CC The nucleic acid encoding the chelon protein is useful for binding CC divalent mercuric ions, to take up, sequester and concentrate the heavy CC irrigation water of waste streams. The DNA of the invention, when CM importance on the invention of the invention or contaminated environment waste streams or contaminated considered in a solid support. Is useful for concentrating heavy metal aqueous medium including biological fluids. The nucleic acid, when creombinantly expressed in enteric bacteria (which are nontoxigenic and celmination of mercuric ion from gastrointestinal tracts of animals or humans exposed to toxic metal ions such as mercury and/or cadmium. The molecules of the invention are also useful in water treatment resins. CC The nucleic acid of the invention is highly specific and binds divalent caid sequence represents the Shigella flexneri wild-type MerR protein of theinvention of heavy metal binding proteins termed chelons.
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Best Local
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                                                                                           Berggren C, BOULILL
The Jakeman K,
שלו
                           WPI; 1999-254424/21
                                                                                     Van Der Lelie D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          25-MAR-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WO9914597-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Heavy metal ion selectivity; metal ion-specific affinity sensor; capacitance measurement; noble metal; self-assembling monolayer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MerR protein which has selectivity towards heavy metal ions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    30-JUN-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAY01816;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY01816 standard; protein; 144 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                 (BERG/) BERGGREN C. (BONT/) BONTIDEAN I
                                                                                                                                                                                                                                                                                                                                                                                                                                            15-SEP-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   15-SEP-1998;
                                                                                                                                                                                                                                                                                                                         (CSOE/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          mercury; cadmium; copper; lead; environmental sample; medicine;
                                                                                                                                                                                                                                                                                       ) BONTIDEAN I.
) CSOEREGI E.
) JOHANSSON G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    l Similarity
56; Conserv
                                                                                                                                                                             MATTIASSON B.

MATTIASSON B.

UNIV BIRMINGHAM SCHOOL BIOLOGICAL SCI.

UNAMAGE INSTELLING TECHNOLOGISCH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  144 AA;
                                                                                                          Bontidean I, Brown N, akeman K, Johansson G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                         97SE-0003315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                98WO-SE01638.
                                                                                     Wilson J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         47.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 290; DB 23;
Pred. No. 3.8e-21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                          Corbisier
Lloyd J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     DB 23;
                                                                                                             P, Csoere
Mattiasson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 144;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                          Csoeregi E;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
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RESULT 12
AAR49668
ID AAR49
XX AAR49
AC AAR49
AC AAR49
XX Fesis
XX Fesis
XX Thiob
XX
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           invention. The specification describes a metal ion-specific, affinity sensor that measures capacitance. The sensor comprises a piece of noble metal to which are bound groups that bind specifically to selected heavy metal ions. These groups are bound to a self-assembling monolayer that covers at least 90% more preferably at least 99% of the noble metal surface. The noble metal is a rod or piece of insulating material (91ass, quartz or silica) on which a noble metal is sputtered. The sensor is used for qualitative or quantitative detection of selected heavy metal ions in liquid samples, particularly of zinc, mercury, cadmium, copper and lead in e.g. environmental samples, medicines, foods and other products.
                                                                                                                                                Sequence
                                                                                                                                                                                                                                       used to transform other bacteria
                                                                                                                                                                                                                                                                              The mercury resistance genes can be used as selectable markers when
                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 2; 26pp; Japanese
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mercury resistant control gene merR and shuttle vector - for enhanced expression of mercury resistance marker in transformed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Thiobacillus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N-PSDB; AAQ58554.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1994-077131/10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17-JAN-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17-JAN-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11-JAN-1994.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Thiobacillus ferrooxidans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               16-SEP-1994 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAR49668 standard; Protein; 159 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Resistance;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Protein product of mercury resistance control gene merR(1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (DOWA ) DOWA MINING CO LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (AKIT-) AKITA KEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           transformation; detection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present sequence represents a protein that is selective towards heavy metal ions. It is used in the construction of the sensor of the sens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 8; Page 22-23; 40pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Capacitance sensor specific for heavy metal ions
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  similarity 93.0%;
                                                                                                                                                159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   144 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      mercury; selectable marker; Thiobacillus ferrooxidans;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                                                                                                                                                A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      91JP-0018338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      91JP-0018338
    41.9%;
76.9%;
Score 257; DB 15;
Pred. No. 7.9e-18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 276; DB 20;
Pred. No. 9.2e-20;
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                                                Length 159;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 144;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
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Matches

50;

Conservative

6,

Mismatches

Indels

0

Gaps

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RESULT 14
AAR49670
ID AAR49
XX
AC AAR49
XX
DE Prote
XX
KW Resis
KW Resis
XX
XX
Thiob
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local S
Matches 24
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The mercury resistance genes can be used as selectable markers when used to transform other bacteria.  \label{eq:constraint} % \begin{array}{c} (x,y) & 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Protein product of mercury resistance control gene merR(2).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 3; 26pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Thiobacillus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mercury resistant control gene merR and shuttle vector - for enhanced expression of mercury resistance marker in transform
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 N-PSDB; AAQ58555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1994-077131/10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17-JAN-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     17-JAN-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11-JAN-1994.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         transformation; detection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Resistance; mercury; selectable marker; Thiobacillus ferrooxidans;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16-SEP-1994 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAR49669;
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                         Thiobacillus ferrooxidans
                                                                                                                                                             Protein product of mercury resistance control gene merR(3).
                                                                                                                                                                                                                      16-SEP-1994 (first entry)
                                                                                                                                                                                                                                                                             AAR49670
                                                                                                                                                                                                                                                                                                                                   AAR49670 standard; Protein; 135
                                                                             Resistance; mercury; selectable marker; Thiobacillus ferrooxidans; transformation; detection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (AKIT-) AKITA KEN.
(DOWA ) DOWA MINING CO LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          140 GDRAT 144
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         76
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 THCEEASSLAEHKLKDVREKMADLARMETVLSELVCACHARKGNVSCPLIASLQ 55
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             135 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20.4%; Score 125; DB 15; ilarity 44.4%; Pred. No. 7.5e-05; Conservative 13; Mismatches 17;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    91JP-0018338
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 135;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0
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ABP38137
ID ABP38
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PXPXPXS
ABN90538 to ABN93374 represent Staphylococcus epidermidis open reading frame (ORF) nucleic acid sequences which encode the amino acid sequences given in ABP35124 to ABP37960. The S. epidermidis sequences have
                                                                                                               Disclosure; SEQ ID 2982; 267pp; English.
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SQ CCCC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The mercury resistance genes can be used as selectable markers when used to transform other bacteria. % \left( 1\right) =\left\{ 1\right\} =\left\{ 1
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Novel isolated nucleic acid encoding a Staphylococcus epidermidis polypeptide, useful for diagnosing and treating bacterial infections -
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08-NOV-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Staphylococcus epidermidis.
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(DOWA ) DOWA MINING CO LTD.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                            antibacterial activity and can be used in gene therapy. The sequences can also be used in the diagnosis and treatment of bacterial infections, particularly S. epidermidis infections. The sequences can be used to screen for compounds able to interfere with the S. epidermidis life cycle or inhibit S. epidermidis infection.

N.B. The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from the
                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence
                                                                                      124 YTCP 127
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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regulatory protein merk - recurrence.
C;Species: Pseudomonas sp.
C;Date: 07-May-1995 #sequence_revision 19-Oct-1995 #text_change 20-Sep-1999
C;Accession: S51755
C;Accession: S51755
                                                                                                                                                                                       A; Description: Sequence con
A; Reference number: S51703
A; Accession: S51749
                                                                                                                                                                                                                                                                                          regulatory protein merR - Pseudomonas fluorescens C;Species: Pseudomonas fluorescens C;Species: Pseudomonas fluorescens C;Date: 07-May-1995 #sequence_revision 19-Oct-1995 #text_change 24-May-2001 C;Accession: S51749
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C;Species: Enterobacter aerogenes
C;Date: 07-May-1995 #sequence_revision 19-Oct-1995 #text_change 20-Sep-1999
                                                                                                                        A; Molecule type: DNA
A; Residues: 1-144 < OSB>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Cross-references: EMBL:Z33488; NID:g607071; PIDN:CAA83896.1; PID:g607072 C;Superfamily: transcription repressor glnR
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A; Residues: 1-144 <OSB>
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A; Accession: S51720
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                                                                           C; Superfamily: transcription repressor gink
                                                                                                     A;Cross-references: EMBL:Z33490; NID:g607153; PIDN:CAA83898.1; PID:g607154
                                                                                                                                                                 A;Status: preliminary
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A; Residues: 1-144 <OSB>
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Pred. No. 1.4e-18;
2; Mismatches 2;
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Pred. No. 6e-19;
                   Score 276; DB 2; Pred. No. 1.4e-18;
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C;Species: Xanthomonas sp.
C;Date: 08-Dec-1993 #sequence_revision 01-Dec-1995 #text_change 20-Sep-1999
C;Accession: S32798; S70142
R;Kholodii, G.Y.; Yurieva, O.V.; Lomovskaya, O.L.; Gorlenko, Z.M.; Mindlin, J. M. Biol. 230, 1103-1107, 1993
A;Title: Tn5053, a mercury resistance transposon with integron's ends.
A;Reference number: S32795; MUID:93253772; PMID:8387603
A;Accession: S32798
                                                                                                                                                                                                                                                                                                                                               A;Cross-references: EMBL:L03729; NID:g1019671; PIDN:AAA98396.1; PID:g154910
A;Experimental source: plasmid RP1; transposon Tn5053
R;Kholodii, G;Y.; Mindlin, S.Z.; Bass, I.A.; Yurieva, O.V.; Minakhina, S.V.; Nikiforo Mol. Microbiol. 17, 1189-1200, 1995
Mol. Microbiol. 17, 1189-1200, 1995
A;Title: Four genes, two ends, and a res region are involved in transposition of Tn50
A;Reference number: S70140; MUID:96130850; PMID:8594337
A;Accession: S70142
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A;Title: The sequence of the mer operon of pMER327/419 and transposon A;Reference number: 139574; MUID:94341572; PMID:8063107
A;Accession: I39574
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C;Date: 19-Jul-1996 #sequence_revision 19-Jul-1996 #text_change 20-Sep-1999
C;Accession: I39574; S37035
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C;Superfamily: transcription repressor glnR
                                                                                    A; Mobile element: transposon Tn5053
C; Superfamily: transcription repressor glnR
                                                                                                                                              A; Gene: merR
                                                                                                                                                                                                       A;Cross-references: EMBL:L40585; NID:g710572; A;Note: the nucleotide sequence was submitted
                                                                                                                                                                                                                                                                    A; Molecule type: DNA
A; Residues: 1-144 <KH2>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Cross-references: EMBL:Z23094; GB:L20693; NID:g388553; PIDN:AAB05979.1; PID:g388554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Molecule type: DNA
A; Residues: 1-144 < RES>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   mer operon regulator - Alcaligenes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               140 SADA 143
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               80 THCEEASSLAEHKLKDVRERMADLARMEAVLSDLVCACHARKGNVSCPLIASLQGKKEPR 139
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 THCEEASSLAEHKLKDVREKMADLARMETVLSELVCACHARKGNVSCPLIASLQGSSGTH 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Xanthomonas sp. transposon Tn5053
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          44.5%;
82.8%;
82.8%;
                              44.5%;
   Score 273; DB 2;
Pred. No. 2.7e-18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 273; DB 2;
Pred. No. 2.7e-18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                          PIDN:AAA98322.1;
to the EMBL Data
                              Length 144;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 144;
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                                                                                                                                                                                                          PID:g710575
Library, May 1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ends
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Conservative

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Mismatches

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Indels

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Gaps

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regulatory protein merR - Pseudomonas fluorescens
N;Alternate names: mer operon regulator
C;Species: Pseudomonas fluorescens
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 20-Sep-1999
C;Accession: S37044
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                                                                                                                                                                                                                                                      Q
                                                                                                                                                                                                                                                                                                                       В
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A;Residues: 1-144 <HOB>
A;Cross-references: EMBL:Z23095; NID:g397617; PIDN:CAA80641.1; PID:g397618
C;Superfamily: transcription repressor glnR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  submitted to the EMBL Data Library, June 1993
A;Description: The nucleotide sequence of the mer operon of pMJ100 and transposon ends
A;Reference number: S37035
      regulatory protein merR - Acinetobacter calcoaceticus (isolate SE11 and SE12)
                                                                                      RESULT 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Status: preliminary
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A:Cross-references: EMBL:Z33481; NID:g607169; PIDN:CAA83889.1; PID:g607170 A;Note: the source is given as Pseudomonas testosteroni C;Superfamily: transcription repressor glnR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Description: Sequence conservation between regulatory mercury resistance genes from me
A;Reference number: S51703
A;Accession: S51756
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Accession: $51756
R;Osborn, A.M.; Bruce, K.D.; Strike, P.; Ritchie, D.A. submitted to the EMBL Data Library, May 1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    regulatory protein merR - Comamonas testosteroni C;Species: Comamonas testosteroni C;Date: 07-May-1995 *sequence_revision 10-Nov-1995 *text_change 20-Sep-1999 C;Date: 07-May-1995 *sequence_revision 10-Nov-1995 *text_change 20-Sep-1999 **Commonas testosteroni C;Date: 07-May-1995 **Sequence_revision 10-Nov-1995 **Text_change 20-Sep-1999 **Commonas testosteroni C;Species: 07-May-1995 **Sequence_revision 10-Nov-1995 **Text_change 20-Sep-1999 **Commonas testosteroni C;Date: 07-May-1995 **Sequence_revision 10-Nov-1995 **Text_change 20-Sep-1999 **Text_change 20-Sep
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: DNA
A; Residues: 1-144 < OSB>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
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                                                                                                                                                                                       140 SADA 143
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2 THCEEASSLAEHKLKDVREKMADLARMETVLSELVCACHARKGNVSCPLIASLOGSSGTH 61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      J.; Kholodii, G.; Nikiforov, V.; Ritchie, D.A.; Strike, P.; Yurieva, O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            THCEEASSLAEHKLKDVRERMADLARMEAVLSDLVCACHARKGNVSCPLIASLQGKKEPR 139
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                             3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 273; DB 2;
Pred. No. 2.7e-18;
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                                                                                                                                                                                                                                                                                                                                                                                                                                          0;
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regulatory protein merR - Klebsiella oxytoca

C;SpecLes: Klebsiella oxytoca

C;Date: 07-May-1995 #sequence_revision 01-Sep-1995 #text_change 20-Sep-1999

C;Accession: S51705
                                                                                                                                       RESULT 12
S51705
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Molecule type: DNA A; Residues: 1-151 < 0SB>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Date: 07-May-1995 #sequence_revision 19-Oct-1995 #text_change 20-Sep-1999
C;Accession: S51721
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              regulatory protein merR - Enterobacter cloacae C; Species: Enterobacter cloacae
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C; Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Cross-references: EMBL:Z33483; NID:g607034; PIDN:CAA83891.1; PID:g607035
A;Experimental source: isolate SE12
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A; Accession: S51703
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            C;Species: Acinetobacter calcoaceticus
A;Variety: isolate SE11; isolate SE12
C;Date: 07-May-1995 #sequence_revision 01-Sep-1995 #text_change 20-Sep-1999
C;Accession: S51703; S51704
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Residues: 1-151 < OSO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: DNA
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                                                                                                                                                                                                                                                                                                                                  62 CEEASSLAEH 71
                                                                                                                                                                                                                                                                                                                                                                                         80 THCEEASGLAEHKLKDVREKNADLARMEAVLSELVCACHARKGNVSCPLIASLQ--DGTK 137
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            44.0%;
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81.4%;

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    Mismatches

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Pred. No. 5.9e-18;
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Pred. No. 5.9e-18;
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Indels Length 151;

3,

Gaps

2

Length 151; Indels

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Gaps

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R;Osborn, A.M.; Bruce, K.D.; Strike, P.; Ritchie, D.A. submitted to the EMBL Data Library, May 1994
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A; Accession: S51705
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A; Cross-references: EMBL: 233485; NID: 9607036; PIDN: CAA83893.1; PID: 9607037
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C;Species: Agrobacterium radiobacter
C;Date: 07-May-1995 #sequence_revision 01-Sep-1995 #text_change 20-Sep-1999
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A;Genome: plasmid
C;Superfamily: transcription repressor glnR
C;Keywords: DNA binding; transcription regulation
                                                                                                                                                                                                                                                                                                                                       merR protein - Escherichia coli plasmid pDU1358
C;Species: Escherichia coli
C;Date: 09-Mar-1990 #sequence_revision 09-Mar-1990 #text_change 20-Sep-1999
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A; Accession: S51707
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R;Osborn, A.M.; Bruce, K.D.; Strike, P.; Ritchie, D.A.
submitted to the EMBL Data Library, May 1994
                                                                                                                                                                                            A;Title: Mercury operon regulation by the merR gene of the organomercurial resistance sya, Reference number: A33858; MUID:89327136; PMID:2666393
A;Accession: A33858
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: EMBL:Z33487; NID:g607040; PIDN:CAA83895.1; PID:g607041
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A; Residues: 1-151 <OSB>
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R; Nucifora, G.; Chu,
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                                                                           C; Genetics:
                                                                                                  A;Cross-references: GB:M24940; NID:g150631; PIDN:AAA98221.1; PID:g455313
                                                                                                                        A; Molecule type: DNA
A; Residues: 1-144 < NUC>
                                                                                                                                                                        A;Status: preliminary
                                                                                                                                                                                                                                                                   R; Nucifora, G.; Chu, L.; Silver, S.; Misra, T.K.
| Bacteriol. 171, 4241-4247, 1989
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Best Local 9
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Residues: 1-151 <OSB>
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Best Local :
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                                                  plasmid
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81.48;
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Pred. No. 5.9e-18;
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pred. No. 1.1e-17;
2; Mismatches 9; Indels 3
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A;Molecule type: DNA
A;Residues: 1-135 <INO>
A;Cross-references: EMBL:X57326; NID:g48150; PIDN:CAA40603.1; PID:g48157
C;Superfamily: transcription repressor glnR
                                                                                                                                                                                                                                                                                                                                   mol. Microbiol. 5, 2707-2718, 1991
A;Title: The merR regulatory gene in Thiobacillus ferrooxidans is spaced apart from A;Reference number: S18584; MUID:92140035; PMID:1779760
A;Accession: S18590
A;Accession: S18590
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C;Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 20-Sep-1999
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Search completed: May 28, 2003, 10:29:15 Job time : 18 secs
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Best Local Similarity
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Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein - Thiobacillus ferrooxidans
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                                                                                                                          2 THCEEASSLAEHKLKDVREKMADLARMETVLSELVCACHARKGNVSCPLIASLQ 55
                                                                                                                                                                 24;
                                                                                                                                                                                       Similarity
                                                                                                                                                               llarity 44.4%; Pred. No. 0.00 Conservative 13; Mismatches
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92.78;
                                                                                                                                                                                20.4%; Score 125; DB 2; Length 135;
44.4%; Pred. No. 0.00012;
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Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries Database : Minimum DB seq length: 0
Maximum DB seq length: 2000000000 Minimum Total number of hits satisfying chosen parameters: Title: Perfect score: OM protein - protein search, using sw model Scoring table: Sequence: Run on: Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. May 28, 2003, 10:25:27; Search time 12 Seconds (without alignments) 404.394 Million cell updates/sec 112892 seqs, 41476328 residues BLOSUM62 US-09-977-137A-4 613 Gapop 10.0 , Gapext 0.5 SwissProt_40:* MTHCEEASSLAEHKLKDVRE.....HARKGNVSCPSAWSHPQFEK 117 GenCore version 5.1.4_p5_4578 Copyright (c) 1993 - 2003 Compugen Ltd. SUMMARIES 112892

320 32 33 33 31	Result No.
260 260 260 83 83 83 79 79 75 75 75 75 75 77 72 72 72 72 72 72 71 71 71 71 71 71 71 70 70 70 70 70 70 70 70 70 70 70 70 70	Score 290
45. 42. 113. 122. 95. 112. 113. 114. 115. 116. 116. 117.	Query Match I
1144 1144 1132 1132 1141 11727 1139 1139 1139 1139 1139 1234 1234 1234 1234 1234 1234 1234 1234	Length DB
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ALIGNMENTS

88888888	466666666666666666666666666666666666666	RP RA	RA RA RA RT RT	RA RA RA	RESULT MERR_S ID MAC P AC P DT 0 DT 1 DT 1 DE MS GN MS GN MS GS
This SWISS-PROT entry is copyright. It is produced through a collaboratio between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as long as its content is in no wa modified and this statement is not removed. Usage by and for commercia entitles requires a license agreement (See http://www.isb-sib.ch/announce, or send an email to license@isb-sib.ch).	O MOI. APPL. Genet. 2:601-619(1944). FUNCTION: MEDIATES THE MERCURY-DEPENDENT INDUCTION OF MERCURY RESISTANCE OPERON. IN THE ABSENCE OF MERCURY MERR REPRESSES TRANSCRIPTION BY BINDING TIGHTLY TO THE MER OPERATOR REGION; WHEN MERCURY IS PRESENT THE DIMERIC COMPLEX BINDS A SINGLE ION AND BECOMES A POTENT TRANSCRIPTIONAL ACTIVATOR, WHILE REMAINING BOUND TO THE MER SITE. TRANSCRIPTIONAL ACTIVATOR, WHILE REMAINING REGULATORS.	SEQUENCE FROM N.A. SPECIES-S.flexneri; PLASMID-IncFII NR1; TRANSPOSON-Tn21; MEDLINE-85159407; PubMed-6530603; Barrineau P., Gilbert P., Jackson W.J., Jones C.S., Summers A.O., Wisdom S.; "The DNA sequence of the mercury resistance operon of the IncFII plasmid NR1.";	T., Hamlin N., Larsen T.S., Larsen T.S., Rutherford d.S., Barrell d.S., Barrell e genome sequeserovar Typh 13:848-852(20	01, 623; M.A. M.A. phi; STRAIN=CT18; PLASMID=pHCM1; phi; STRAIN=CT18; PLASMID=pHCM1; phi; STRAIN=CT18; PLASMID=pHCM1; 4947; PubMed=11677608; LOUGAN G., James K.D., Thomson N.R., Pickard D., Walley S.D., Holden M.T.G., Sebaihia Mungall K.L., Bentley S.D., Holden M.T.G., Sebaihia Sham D., Brooks K., Chillingworth T., Connerton P., avis P., Davies R.M., Dowd L., White N., Farrar J.,	_SALTI _SALTI STANDARD; PRT; 144 AA. P07044; P07044; O1-APR-1988 (Rel. 07, Created) O1-APR-1988 (Rel. 07, Last sequence update) 15-JUN-2002 (Rel. 41, Last annotation update) Mercuric resistance operon regulatory protein. MERR OR HCM1.235. Salmonella typhi, and Shigella flexneri. Plasmid pHCM1, and Plasmid IncFII NR1. Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae; Salmonella.

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SMART; SM00422; HTH_MERR; 1.
PROSITE; PS00552; HTH_MERR, FAMILY; 1.
Transcription regulation; Activator; Repressor; Mercuric resistance; Mercury; DNA-binding; Plasmid; Transposable element;
                                                                    Shewchuk L.M., Verdine G.L., Nash H., Walsh C.T.;

"Mutagenesis of the cysteines in the metalloregulatory protein Merr

indicates that a metal-bridged dimer activates transcription.";

Biochemistry 28:6140-6145(1989).

1- FUNCTION: MEDIATES THE MERCURIC-DEPENDENT INDUCTION OF MERCURY

RESISTANCE OPERON. IN THE ABSENCE OF MERCURY MERR REPRESSES

TRANSCRIPTION BY BINDING TIGHTLY TO THE MER OPERATOR REGION;

WHEN MERCURY IS PRESENT THE DIMERIC COMPLEX BINDS A SINGLE ION

AND BECOMES A POTENT TRANSCRIPTIONAL ACTIVATOR, WHILE REMAINING

BOUND TO THE MER SITE.
                                                                                                                                                                                                                                                                                                                                         Misra T.K., Brown N.L., Fritzinger D.C., Pridmore R.D., Barnes W.M., Haberstroh L., Silver S.; Mercuric ion-resistance operons of plasmid R100 and transposon Tn501: the beginning of the operon including the regulatory region and the first two structural genes."; Proc. Natl. Acad. Sci. U.S.A. 81:5975-5979(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pseudomonas aeruginosa, and Pseudomonas fluorescens plasmid pVS1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-JAN-1988 (Rel. 06, Created)
01-JAN-1988 (Rel. 06, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation updat
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This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EN
                                                                                                                                                                                                                                                                   Osborn A.M., Bruce K.D., Submitted (DEC-1994) to
                                                                                                                                                                                                                                                                                                                                                                                                                                                 TRANSPOSON-Tn501;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mercuric resistance operon regulatory protein
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                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pseudomonas
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                                                         SIMILARITY: BELONGS TO THE MERR FAMILY OF TRANSCRIPTIONAL
                                           REGULATORS.
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                                                                                                                                                                                                                                                                    the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                 Strike P., Ritchie D.A.;
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HG(2+).
HG(2+).
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pred. No. 1.9e-20;
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Best Local (
                                                                                                                                                               Nucifora G., Chu L., Silver S., Misra T.K.;

"Mercury operon regulation by the merR gene of the organomercurial resistance system of plasmid pDU1358.";

J. Bacteriol. 171:4241-4247(1989).

1- FUNCTION: MEDIATES THE MERCURIC-DEPENDENT INDUCTION OF MERCURY RESISTANCE OPERON. IN THE ABSENCE OF MERCURY MERR REPRESSES TRANSCRIPTION BY BINDING TIGHTLY TO THE MER OPERATOR REGION; WHEN MERCURY IS PRESENT THE DIMERIC COMPLEX BINDS A SINGLE ION AND BECOMES A POTENT TRANSCRIPTIONAL ACTIVATOR, WHILE REMAINING BOUND TO THE MER SITE.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-JAN-1990 (Rel. 13, Created)
01-JAN-1990 (Rel. 13, Last sequence update)
01-CCT-1993 (Rel. 27, Last annotation update)
Mercuric resistance operon regulatory protein
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Transcription regulation; Activator; Repressor; Mercuric resistance;
Mercury; DNA-binding; Plasmid; Transposable element.
This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. MEDLINE=89327136; PubMed=2666393;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Plasmid pDU1358
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                                                                                                                        REGULATORS.
                                                                                                                                                  SIMILARITY: BELONGS
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SM00422; HTH_MERR; 1.
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93.0%;
                                                                                                                                                     TO THE MERR FAMILY OF TRANSCRIPTIONAL
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Pred. No. 3.
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C->S: ABOLI
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                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                      operon from Staphylococcus aureus plasmid p1258.";
Proc. Natl. Acad. Sci. U.S.A. 84:5106-5110(1987).
-I- FUNCTION: MEDIATES THE MERCURIC-DEPENDENT INDUCTION OF MERCURY RESISTANCE OPERON. IN THE ABSENCE OF MERCURY MERR REPRESSES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-AUG-1991 (Rel. 19, Created)
01-AUG-1991 (Rel. 19, Last sequence update)
01-OCT-1993 (Rel. 27, Last annotation updat
             PRINTS; PR00040; HTHMERR. SMART; SM00422; HTH_MERR; 1.
                                                                        EMBL; L29436; AAA98241.1; -. PIR; A29504; A29504.
                                                                                                                 entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                              use by non-profit institutions as long as modified and this statement is not removed. (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Firmicutes; Bacillales; Staphylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Staphylococcus aureus
                                            InterPro; IPR000551;
Pfam; PF00376; merR;
                                                                                                                                                                                                                                                                                                                                                                                              Laddaga R.A., Chu L., Misra T.K., Silver S.;
"Nucleotide sequence and expression of the mercurial-resistance
                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=87260937; PubMed=3037534;
                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Plasmid pI258
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P22874;
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SMART; SM00422; HTH_MERR; 1.
PROSITE; PS00552; HTH_MERR_FAMILY; 1.
Transcription regulation; Activator; Repressor; Mercuric resistance;
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Pfam; PF00376; merr; 1.
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SUBUNIT: HOMODIMER.
SIMILARITY: BELONGS TO THE MERR FAMILY OF TRANSCRIPTIONAL
                                                                                                                                                                                                                                                                                            TRANSCRIPTION BY BINDING TIGHTLY TO THE MER OPERATOR REGION; WHEN MERCURY IS PRESENT THE DIMERIC COMPLEX BINDS A SINGLE ION AND BECOMES A POTENT TRANSCRIPTIONAL ACTIVATOR, WHILE REMAINING
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HTH_MERR_FAMILY; 1.
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92.7%;
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HG(2+).
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protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DB 1; Length 144; .2e-17;
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                                                                                                                                            Usage
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SQ FTT FTW SQ
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Best Local
                                                                                                                                                                                                                                                                                          Helmann J.D., Ballard B.T., Walsh C.T.;
"The MerR metalloregulatory protein binds mercuric ion tricoordinate, metal-bridged dimer.";
                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=89123021; PubMed=2492496;
Helmann J.D., Wang Y., Mahler I., Walsh C.T.;
"Homologous metalloregulatory proteins from both Gram-positive and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDLINE-89123092; PubMed=2536669; Walsh C., Mahler I.; Wang Y., Moore M., Levinson H.S., Silver S., Walsh C., Mahler I.; "Nucleotide sequence of a chromosomal mercury resistance determination a Bacilus sp. with broad-spectrum mercury resistance.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-AUG-1991 (Rel.
01-AUG-1991 (Rel.
01-OCT-1993 (Rel.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              METAL
METAL
                                                                                                                                                                                                                                                                                                                                                                                               Gram-negative bacteria control transcription of mercury
                                                                                                                                                                                                                                                                               Science 247:946-948(1990)
                                                                                                                                                                                                                                                                                                                                 MEDLINE=90161989; PubMed=2305262;
                                                                                                                                                                                                                                                                                                                                                MUTAGENESIS
                                                                                                                                                                                                                                                                                                                                                                                   operons.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   FUNCTION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NCBI_TaxID=1420;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Bacillus sp. (strain RC607).
Bacteria; Firmicutes; Bacillales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mercuric resistance operon regulatory protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     P22853;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Transcription regulation; Activator; Repressor; Mercuric resistance;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              79 CKDMYAFTVQKTKEIERKVQGLLRIQRLLEELKEKCPDEKAMYTCPIIETLMG 131
                                                                                                                                                                                                                                                                                                                                                                       Bacteriol. 171:222-229(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bacteriol. 171:83-92(1989).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       4 CEEASSLAEHKLKDVREKMADLARMETVLSELVCACHARKGNVSCPLIASLQG
                                                                                                                                                                                                   FUNCTION: MEDIATES THE MERCURIC-DEPENDENT INDUCTION OF MERCURY RESISTANCE OPERON. IN THE ABSENCE OF MERCURY MERR REPRESSES TRANSCRIPTION BY BINDING TIGHTLY TO THE MER OPERATOR REGION; WHEN MERCURY IS PRESENT THE DIMERIC COMPLEX BINDS A SINGLE ION AND BECOMES A POTENT TRANSCRIPTIONAL ACTIVATOR, WHILE REMAINING BOUND TO THE MER SITE.
                                                                                                                                                                       SUBUNIT: HOMODIMER.
SIMILARITY: BELONGS TO THE MERR FAMILY OF TRANSCRIPTIONAL
                                                                                                                                                                  REGULATORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  16;
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135
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             19, Created)19, Last sequence u27, Last annotation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13.5%;
30.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  15741 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 83;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HG(2+)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FDC1A852621D4F82 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bacillaceae; Bacillus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             update)
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                                                                                                                                                                                                                  WHILE REMAINING
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s requires a license agreement (See http://www.isb-sib.ch/announce/ an email to license@isb-sib.ch).

PIR; A32239; A32239

InterPro;

IPR000551;

HTH_MerR

EMBL; AF138877; AAA83973.1; PIR; A32227; A32227.

or send entities

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RESULT 6
ZNTR_ECOLI
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Matches
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01-JUN-1994 (Rel. 29, Last sequence update)
01-JUN-1994 (Rel. 29, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
2n(II) responsive regulator of zntA.
ZNTR OR B3292 OR Z4662 OR ECS4157.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MUTAGEN
MUTAGEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            METAL
METAL
MUTAGEN
                                                                                                                      STRAIN-0157:H7 / EDL933 / ATCC 700927;

MEDLINE-21074935; PubMed-11206551;

Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,

Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,

Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,

Grotbeck E.J., Davis N.W., Lim A., Dinalanta E.T., Potamousis K.,

Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,

Welch R.A., Blattner F.R.;

"Genome sequence of enterohaemorrhagic Escherichia coli 0157:H7.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRINTS; PR00040; HTHMERR. SMART; SM00422; HTH_MERR; 1.
SEQUENCE FROM N.A.

STRAIN-0157:H7 / RIMD 0509952;

STRAIN-0157:H7 / RIMD 0509952;

Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Hayashi T., Makino E., Nakayama K., Murata T., Tanaka M., Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Y
                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.

MEDLINE-94341562; PubMed-8063098;

Christie G.E., White T.J., Goodwin T.S.;

A merk homologue at 74 minutes on the E.

Gene 146:131-132(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00376; merR; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Escherichia coli, and Escherichia coli 0157:H7.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PROSITE; PS00552; HTH_MERR_FAMILY; 1.
                                                                                                                                                                                                                                                                                            "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                     MEDLINE-97426617; PubMed-9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V., Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
STRAIN-K12 / MG1655;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         METAL
                                                                                                            Nature 409:529-533(2001).
                                                                                                                                                                                                                                                                                                                            Mau B.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZNTR_ECOLI
                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=562, 83334;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 CEEASSLAEHKIKDVREKMADLARMETVLSELVCACHARKGNVSCPLIASL 54
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CRDMYDFTILKIEDIQRKIEDLKRIERMLMDLKERCPENKDIYECPIIETL 129
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123
132 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15971 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   gamma subdivision; Enterobacteriaceae;
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HG(2+).
HG(2+).
HG(2+).
C->A, H: LOSS OF HG
C->A, H: LOSS OF HG
C->A, H: LOSS OF HG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6557FBF1FB95B635 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Escherichia coli genome.";
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   Yasunaga T.
                    Tobe T.,
                                 Yokoyama K.,
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SQ TWREET BREET BR
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Best Local S
Matches 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                    MEDLINE=21848401; PubMed=11859360; Wood V., Gwilliam R., Rajandream M.A., Lyne M., Lyne R., Stewart A., Syouros J., Peat W., Hayles J., Baker S., Basham D., Bowman S., Stevard R., Brown D., Brown S., Chillingworth T., Churcher C.M., Collins M., Connor R., Cronin A., Davis P., Feltwell T., Fraser A., Gentles S., Goble A., Hamlin N., Harris D., Hidalgo J., Hodgson G., Holroyd S., Hornsby T., Howarth S., Huckle E.J., Hunt S., Jagels K., James K., Jones L., Jones M., Leather S., McDonald S., McLean J., James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q9UTK5; 013313; Q9UTT8;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation updat
Abnormal long morphology protein 1 (Sp8)
ALMI OR SPAC1486.04C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; L29458;
EMBL; U18997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Brocklehurst K.R., Hobman J.L., Lawley B., Blank L., Marshall S.J., Brown N.L., Morby A.P.;
"ZntR is a Zn(II)-responsive MerR-like transcriptional regulator of
                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Fungi; Ascomycota; Schizosaccharomycete Schizosaccharomycetales; Schizosaccharomycetaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                        Schizosaccharomyces pombe (Fission yeast).
Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SCHPO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AE000407; AAC76317.1; -. EMBL; AE005556; AAG58413.1; -. EMBL; AP002564; BAB37580.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                     STRAIN-972;
                                                                                                                                                                                                                                                                                                                                                                  Schizosaccharomyces.
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                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=4896;
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les 18; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CQESKGIVQERLQEVEARIAELQSMQRSLQRLNDACCGTAHSSVYCSILEALEQGASG
Moule S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PubMed=10048032;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12.9%;
31.0%;
Mungall K., Murphy L., Niblett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 79;
Pred. No. 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  update)
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RA Skelton J., Simmonds M., Squares R., Squares S., Stevens K.,

RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,

RA Woodward J., Volckaert G., Aert R., Robben J., Grymonprez B.,

RA Weltjens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,

RA Gabel C., Fuchs M., Filtzc C., Holzer E., Moestl D., Hilbert H.,

RA Borzym K., Langer I., Beck A., Lehrach H., Reinhardt R., Pohl T.M.,

RA Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,

RA Eger P., Zimmermann W., Wedler H., Wambutt R., Purnelle B.,

RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,

RA Galibert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,

RA Lucas M., Rochet M., Gaillardin C., Tallada V.A., Garzon A., Thode G.,

RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,

RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,

RA Cerrutti L., Lowe T., McCombie W.R., Paulsen I., Potashkin J.,

RA Shpakovski G.V., Ussery D., Barrell B.G., Nurse P.;

RI Theyer Als, R371-280/3002
                                                                                                                                                Matches
                                                                                                                                                                                Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Large-scale screening of intracellular protein localization in living fission yeast cells by the use of a GFP-fusion genomic DNA library."; Genes Cells 5:169-190(2000).

-i- FUNCTION: AFTER THE ONSET OF MITOSIS, AT MID- TO LATE ANAPHASE, CO-LOCALIZES WITH THE MEDIAL ACTIN RING. MAY PLAY A ROLE IN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Jimenez M., Petit T., Gancedo C., Goday C.;
"The alm1+ gene from Schizosaccharomyces pombe encodes a coiled-coil protein that associates with the medial region during mitosis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nature 415:871-880(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Oliver K.,
                                                                                                                                                                                                                                                                                                                                                                                                                           EMBL; AL133357; CAB62414.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Hiraoka Y
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ding D.Q., Tomita Y., Yamamoto A., Chikashige Y., Haraguchi T.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=20223868;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STRAIN-968 h90;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE OF 644-834 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=20123449; PubMed=10660053;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE OF 495-1727 FROM N.A., AND CHARACTERIZATION
                                                                                                                                                                                                                                                           DOMAIN
                                                                                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                              DOMAIN
                                                                                                                                                                                                                                                                                                                                                                       Coiled
                                                                                                                                                                                                                                                                                                                                                                                      EMBL;
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                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                   DOMAIN
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                                                                                                                                                                                                                                                                                                                                                     DOMAIN
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192 EILVQEKSALVSDLASLQSDHSKVCEKL-EVSSRQVQDLEKKLAGLAQQNTELNEKIQLF 250
                                    48
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                                                                                                                                                                 Cocal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CYTOKINESIS.
                                                                                                           EEASSLAEHKLKDVREKMADLARMETVLSELVCACHARKGNVS-----
                                  -------CPLIASLQGSSGTHCEEASSLAEHKLKDVREKMADLARMETVLSELVCAC 97
                                                                        QEQSKIASEQLSIAKDQIEALQNENSHLGEQVQSAHQALSDIEERKKQHMFASSSSRVKE
                                                                                                                                                                                                                                                                                                                                                                                        AB028012;
                                                                                                                                                                                                                                                                                                                                                                                                         AF010473;
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443
542
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                                                                                                                                                Conservative
                                                                                                                                                                                                                     AA;
                                                                                                                                                                                                                                                                                                                                                                                        BAA87316.1;
                                                                                                                                                                                                                                                                                                                                                                                                       AAB65416.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      262:921-930(2000).
                                                                                                                                                                                                                                                         361
463
740
1106
1427
1555
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              license agreement
                                                                                                                                                                                                                       197858
                                                                                                                                                               12.6%;
19.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pearson D., Quail M.A., Rabbinowitsch E.,
                                                                                                                                              26;
                                                                                                                                                                                                                                      COILED COIL (POTENTIAL).
                                                                                                                                                                                                                     MW;
                                                                                                                                                                                                                                                                                                                                                                                                       ALT_INIT
                                                                                                                                                                 Pred. No.
                                                                                                                                                                                Score 77;
                                                                                                                                              Mismatches
                                                                                                                                                                                                                     F820BF8D9C132644 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                DB 1;
                                                                                                                                              49;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Usage by and for
                                                                                                                                                                                Length 1727;
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                                                                                                                                            Gaps
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RESULT 8
CUER_VIBCH
ID CUER_V
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Best Local Similarity
Matches 15; Conserv
                           Query Match
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15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Transcriptional regulator cueR (Copper efflux regulator) (Copper export regulator).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A., Gill S.R., Nelson K.E., Read T.D., Tettelin H., Richardson D., Ermolaeva M.D., Vamathevan J., Bass S., Qin H., Dragoi I., Sellers P., McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O., Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C., Fraser C.M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nature 406:477-483(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=E1 Tor N16961 / Serotype 01;
MEDLINE=20406833; PubMed=10952301;
Heidelberg J.F., Eisen J.A., Nelson W.C., Clayton R.A., Gwinn M.L.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Vibrio cholerae.
Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CUER_VIBCH
                                                                                                                            PRINTS; PR00040; HTHMERR.
SMART; SM00422; HTH_MERR; 1.
PROSITE; PS00552; HTH_MERR_FAMILY; 1.
                                                                                                                                                                                                                                                                                                           use by non-profit institutions as long modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Srivastava B.S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CUER OR VVGR OR VC0974.
                                                                 SEQUENCE
                                                                                               Complete
                                                                                                              Transcription regulation; Activator; DNA-binding; Copper;
                                                                                                                                                                                                               TIGR; VC0974;
                                                                                                                                                                                                                                    EMBL;
                                                                                                                                                                                                                                                  EMBL; AJ277893; CAC21398.1; ALT_INIT.
                                                                                                                                                                                                                                                                                 entities requires a license agreement (S or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                                                                                                                 This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      cholerae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (MAY-2000) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN=Classical Ogawa 395 / ATCC 39541 / Serotype Ol;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NCBI_TaxID=666;
                                                                                 DNA_BIND
                                                                                                                                                                                Pfam; PF00376; merR;
                                                                                                                                                                                                InterPro; IPR000551; HTH_MerR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "DNA sequence of both chromosomes of the cholera pathogen Vibrio
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        251 EQKRSNYS 258
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98 HARKGNVS 105
                                                                                                                                                                                                                                                                                                                                                                                                                              in response to increasing copper concentrations (By simila SUBUNIT: Homodimer (Potential).
SUBCELLULAR LOCATION: Cytoplasmic (Probable).
DOMAIN: It contains a N-terminal DNA binding region and a terminal metal binding region (By similarity).
SIMILARITY: BELONGS TO THE MERR FAMILY OF TRANSCRIPTIONAL SIMILARITY: CHEPAULY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FUNCTION: Regulates the transcription of the copA and cueO genes It detects cytoplasmic copper stress and activates transcription in response to increasing copper concentrations (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                     REGULATORS. CUER SUBFAMILY.
                                                                                                                                                                                                                                 AE004179; AAF94136.1;
                                                                                                 proteome.
                                                              139 AA;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
                                                                 15693 MW;
               12.5%; 28.8%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gamma subdivision; Vibrionaceae; Vibrio
15;
             Score 76.5;
Pred. No. 1.
                                                                                 H-T-H MOTIF (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRT;
                                                                   84CEDED9D411B012 CRC64;
 Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       139 AA
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 17;
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11 AEHKLKDVREKMADLARMETVLSELVCACHARKGNVSCPLIASLQGSSGTHC 62

84

AQEKWQEISRKLSELTMIKQQLEEWIASCPGDQGS-DCPIIEQLKG----HC

130

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ALD DETERMINED TO SERVICE OF SERV
                                                                                                                                                 RA Addams N.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Addams N.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Addams N.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Addams N.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Addams N.D., Celniker S.E., Holt R.A., Evans C.A., Goller R.P.,
RA Goorge R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Brandon R.C., Rogers Y.H.C., Blazel, R.G., Champe M., Pfelffer B.D.,
RA Brandon R.C., Rogers Y.H.C., Blazel, R.G., Champe M., Pfelffer B.D.,
RA Brandon R.C., Rogers Y.H.C., Blazel, R.G., Champe M., Pfelffer B.D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Baltew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Bockova D., Botchan M.R., Bouck J., Brokstein P., Brottler P.,
RA Bockova D., Botchan M.R., Bouck J., Brandari D., Bolshakov S.,
RA Bodson K.C., Besam D.A., Deng E., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Clodek A., Gong E., Gorrell J.H., Gu.Z., Gun P., Harris M.,
RA Glodek A., Gong F., Gorrell J.H., Gu.Z., Gun P., Harris M.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wel M.-H., Ibegwam C.,
RA McLiu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA McLiu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
RA McLand D.R., Nelson K.A., Nixon K., Nusskern D.R., Mesheci A.,
RA Reinert K., Remington K., Saunders R.D.C., Scheeler F., Shen H.,
RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
RA Haris R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
RA Hang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Hang Z.-Y., Wassarman D.A., Weinstock G.M., Weissenbach J.,
RA Hang X., Zhong F.N., Zhong W., Zhang G., Zhou X., Zheng L.,
Per The genome sequence of Drosophila melanogaster.';
Science 287:2185-2195(2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 9
ITBN_DROME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Mandibulata; Pancrustacea; Hexapoda;
Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera;
Muscomorpha; Ephydroidea; Drosophilidae; Drosophila.
NCBI_TaxID=7227;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Q27591; Q9VIG7;
16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           "A novel, tissue specific integrin subunit, beta nu, expressed in the midgut of Drosophila melanogaster.";
Development 118:845-858(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-20196006; PubMed-10731132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-Berkeley
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-94357079;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Integrin beta-nu precursor.
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                                                               FUNCTION: PROBABLY PLAYS A ROLE IN CELL ADHESION.
SUBUNIT: HETERODIMER OF AN ALPHA AND A BETA SUBUNIT.
SUBCELLULAR LOCATION: Type I membrane protein.
SIMILARITY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          endoderm;
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                          LOCATION: Type I membrane protein.
BELONGS TO THE INTEGRIN BETA CHAIN FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PubMed=8076521;
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                                                                                                                                                                                                                                                               Y355_HUMAN
                                                                                                                                                                                                                                                                                        RESULT 10
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local
                                                                                                                                                                                                             Y355_HUN
O15063;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CARBOHYD
CARBOHYD
CARBOHYD
CARBOHYD
                 Homo sapiens (Human).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                        15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Hypothetical protein KIAA0355.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRINTS; PR00011; EGFLAMININ.
ProDom; PD001811; Integrin_B; 1.
SMART; SM00181; EGF; 1.
SMART; SM000187; INB; 1.
SMART; SM00423; PSI; 1.
SMART; SM00327; VWA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bloinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
NCBI_TaxID=9606
                                                                                              KIAA0355.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CARBOHYD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS00022; EGF_1; UNKNOWN, PROSITE; PS01186; EGF_2; UNKNOWN, PROSITE; PS00243; INTEGRIN_BETA; PROSITE; PS50234; VWFA; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FlyBase; FBgn0010395; beta-Int-nu.
InterPro; IPR000561; EGF-like.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EMBL; AE003669;
HSSP; P05106; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pfam;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; L13305; AAC37169.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Integrin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           InterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          [nterPro;
                                                                                                                                                                                                                                                                                                                                                           547 YTGPFCECRECL-----DCDEKLAD-----CFC----GQCVCKYGWS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    nterPro;
                                                                                                                                                                                                                                                                                                                                                                                                       57 SSGTHCEEASSLAEHKLKDVREKMADLARMETVLSELVCACHARKGNVSCPSAWS 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2 THCE---EASSLAEHK--LKDVREKMADLARMETVLSELVCACHARKGNVSCPLIASLQG 56
                                                                                                                                                                                                                                      HUMAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PF00362; integrin_
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IPR002369;
IPR001169;
IPR002049;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            IPR003659; Plexin-like.
IPR002035; VWF_A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
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                                                                                                                                                                                                                                         STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ä,
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725
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12.3%;
26.1%;
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Integrin_beta_C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Laminin_EGF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   в; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         UNKNOWN_4.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Receptor; Transmembrane; Glycoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 75.5; D
Pred. No. 9.5;
.5; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         N-LINKED (GLCNAC. .
E -> G (IN REF. 1).
V -> A (IN REF. 1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   N-LINKED (GLCNAC. ...) (POTENTIAL)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CYTOPLASMIC (POTENTIAL).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INTEGRIN BETA-NU.
EXTRACELLULAR (POTENTIAL)
                   Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   351869D523F07DEB CRC64;
                                                                                                                                                                                                                                      1070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    35;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 799;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    35;
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SO SO
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WN3A_MOUSE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ρy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         entities requires a license agreement (See http://www.lsb-slb.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                               01-AUG-1992 (Rel. 23, Created)
01-AUG-1992 (Rel. 23, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
WNT-3A protein precursor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nagase T., Ishikawa K.-I., Nakajima D., Ohira M., Seki N., Miyajima N., Tanaka A., Kotani H., Nomura N., Ohara O.; "Prediction of the coding sequences of unidentified human genes. VII. The complete sequences of 100 new cDNA clones from brain which can
                                                                                            development -- restricted temporal and spatial patterns in the developing neural tube.";
Genes Dev. 5:381-388(1991).
-i- FUNCTION: LIGAND FOR MEMBERS OF THE FRIZZLED FAMILY OF SEVEN
TRANSMEMBERANE RECEPTORS. WNT-3 AND WNT-3A PLAY DISTINCT ROLES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            code for large proteins in vitro."; DNA Res. 4:141-150(1997).
                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus
                                                                                                                                                                                                                                                                                                                                   Mus musculus (Mouse)
                                                                                                                                                                                                                                                                                                                                                                                                                                                        WN3A_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Hypothetical protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MEDLINE=97349984; PubMed=9205841;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TISSUE-Brain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                    NCBI_TaxID=10090;
                                                                                                                                                                                                                                                                                                                                                      WNT3A OR WNT-3A
                                                                                                                                                                                                                MEDLINE=91160971; PubMed=2001840;
                                                                                                                                                                                                                                     TISSUE=Embryo;
                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                 "Expression of two members of the Wnt family during mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          375 MKEAGCYNGITSRDDFPVTEVLNQVCPSTW 404
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           259 CSQSAAIPEHQLKELNIKIDSALQAYKIALESLGHCEYAMKAGFHLNPKAIEASLQGC--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           60 THCEEASS-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 CEEASSLAEHKLKDVREKMADLARMETVLSELVCAC-HARKGNVSC---PLIASLQGSSG 59
             extracellular matrix.
TISSUE SPECIFICITY: DORSAL PORTION OF THE NEURAL TUBE (DEVELOPING
                                                SUBCELLULAR LOCATION: Possibly secreted and associates with the
                                                                                 CELL-CELL SIGNALING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        --CSEAEAQQTGRRQTPPQPMQCELPTVPVQIGSHFLKGVSFNESAADNLKLKTHTMLQL 374
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AB002353; BAA20812.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                 H., Nusse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1037
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1070 AA; 116047 MW; 2D35C127C5EBA2F7 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                        STANDARD;
AND MESENCHYME TISSUE SURROUNDING THE UMBILICAL
                                                                                                                                                                                                  R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1044
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             555
700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       12.2%;
                                                                                 DURING
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NVSCPSAW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 74.5;
Pred. No. 1
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POLY-PRO.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           POLY-PRO.
                                                                                 MORPHOGENESIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                        352
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         48;
                                                                                 OF.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels 47;
                                                                                 DEVELOPING
                                                                                                 ROLES
                                                                                 NEURAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ALR_TREPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ALR_TREPA
Q56346;
                                                                                                                                                                                                                                                                                                                                                                                                                                              30-MAY-2000 (Rel. 39, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last annotation update)
Lanine racemase (EC 5.1.1.1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
              "Partial sequence of alanine racemase from Treponema pallidum.";
Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Provides the D-alanine required for cell wall
                                                                                                                                                                                                    MEDLINE=98332770; pubMed=9665876; Fraser C.M., Norris S.J., Weinstock G.M., White O., Sutton G.G., Praser C.M., Norris S.J., Weinstock G.M., White O., Sutton G.G., Dodson R., Gwinn M., Hickey E.K., Clayton R., Ketchum K.A., Sodergren E., Hardham J.M., McLeod M.P., Salzberg S., Peterson J., Sodergren E., Hardham J.M., McLeod M.P., Salzberg S., Peterson J., Khalak H., Richardson D., Howell J.K., Chidambaram M., Utterback T., McDopald L., Artiach P., Bowman C., Cotton M.D., Fujii C., Garland S. McDopald L., Artiach P., Bowman C., Cotton M.D., Fujii C., Garland S. Hatch B., Horst K., Roberts K., Sandusky M., Weidman J., Smith H.O.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CARBOHYD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIGNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Developmental protein; Glycoprotein; Signal; Extracellular matrix.
SIGNAL 1 24 POTENTIAL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; X56842; CAA40173.1; -.
                                                                                                                                                                                                                                                                                                                                                                                               Treponema pallidum.
Bacteria; Spirochaetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SMART; SM00097; WNT1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pfam; PF00110; wnt;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MGD; MGI:98956; Wnt3a.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             -!- SIMILARITY: BELONGS TO THE WNT FAMILY.
                                                                  Steiner B.M., Rodes B.;
                                                                                   STRAIN-Nichols
                                                                                                                                                     spirochete.
                                                                                                                                                             "Complete genome sequence of Treponema pallidum, the syphilis
                                                                                                                                                                                                                                                                                                                             STRAIN=Nichols
                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                             NCBI_TaxID=160;
                                                                                                                                                                                                                                                                                                                                                                                                                                   ALR OR TP0681
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRINTS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   InterPro; IPR000970; Wnt_grthfactor
                                                                                                   SEQUENCE OF 1-198 FROM N.A.
                                                                                                                                     Science
                                                                                                                                                                                       Venter J.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181 SAMNRHNNEAGRQAIASHMHLKCKCHGLSGSCEVKTCWWSQPDF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           33 SELVCACHARKGNVSCPLIASLQGSSGT-----HCE---EASSLAEHKLKDVREKMADL- 83
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 biosynthesis (By similarity).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A39532;
                                                                                                                                     281:375-388(1998).
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PS00246; WNT1; 1.
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352 AA;
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87
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25.0%;
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Pred. No.
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N-LINKED (GLCNAC. . .) (POTENTIAL)
; 7ADFC5B38A8EFF63 CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.

-i- FUNCTION: COMPONENT OF THE EXOSOME 3->5 EXORIBONUCLEASE COMPLEX.

REQUIRED FOR THE 3' PROCESSING OF THE 7S PRE-RNA TO THE MATURE
5.8S RRNA. HAS A 3'-5' EXONUCLEASE ACTIVITY (By similarity).

-i- SUBUNIT: COMPONENT OF THE EXOSOME MULTIENZYME RIBONUCLEASE COMPLEX
COMPOSED OF AT LEAST 11 PROTEINS: RRP4, RRP40, RRP41/SK16, RRP42,
RRP43, RRP44/DIS3, PM/SCL-75, RRP46, CSL4 AND PM/SCL-100 (ONLY IN
                                                                                                                                                         Strausberg R.
                                                                                                                                                                                                                                            15-JUN-2002 (Rel. 41, Created)
15-JUN-2002 (Rel. 41, Last sequence update)
15-JUN-2002 (Rel. 41, Last anotation update)
Exosome complex exonuclease RRP41 (EC 3.1.13.-) (Ribosomal RNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBI outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial
                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                 processing protein
                                                                                                                                                                                                                                                                                                                                         MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; AE001242; AAC65644.1; ALT_INIT.
EMBL; U57756; AAB17466.1; ALT_INIT.
HSSP; P10724; 1BD0.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                        RR41_MOUSE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  entitles requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSITE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              InterPro; IPR000821; Ala_racemase
                                                                                                                                                                                                                                                                                                                                                                                                 199
                                                                                                                                                                                                                                                                                                                                                                                                                                                          145
                                                                                                                                                                                                                                                                                                                                                                                                                             106 CP 107
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COFACTOR: Pyridoxal phosphate (By similarity).
PATHWAY: Along with D-alanine-D-alanine ligase, it makes
D-alanine branch of the peptidoglycan biosynthetic route.
SIMILARITY: BELONGS TO THE ALANINE RACEMASE FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LIASLOGSSGTHCEEAS---SLAEHKLKDVREKMADLARMETVLSELV-CACHARKGNVS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                EEISSLIEHRVHTVISERAHIALIARALRQSADTGATCGVHVKIDTGMGRIGCAPDEACA 144
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PF00842; Ala_racemase; 1.
S; PR00992; ALARACEMASE.
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                                                                                                                                                                                                                                                                                                                        STANDARD;
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40312 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 72.5; D
Pred. No. 8.2;
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CATALYTIC BASE SPECIFIC TO L-ALANINE (BY SIMILARITY).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PYRIDOXAL PHOSPHATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CATALYTIC BASE SPECIFIC TO
                                                                                                                                                                     Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus
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Cell wall; Peptidoglycan synthesis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 377;
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Matches

Similarity

32.7%;

Conservative

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Mismatches

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ALD DESCRIPTION OF COLUMN AND DESCRIPTION OF
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      Query Match
Best Local
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Best Local :
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                                                                                                                     EMBL; X99270; CAA67665.1; ... Genew; HGNC:12270; TREX2.
                                                                                                                                                                                                                                           the European Bioinformatics Institute. There are no rest
use by non-profit institutions as long as its content
modified and this statement is not removed. Usage by an
entities requires a license agreement (See http://www.isb-
                                                                                               SEQUENCE
                                                                                                                                                                                                            entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=97254469; PubMed=9099879;
Esposito T., Ciccodicola A., Flagiello L., Matarazzo M.R.
Migliaccio C., Cifarelli R.A., Visone R., Campanile C.,
Mazzarella R., Schlessinger D., D'Urso M., D'Esposito M.;
"Expressed STSs and transcription of human Xq28.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF01138; RNase_PH; 1.
Pfam; PF03725; RNase_PH_C; 1.
Exosome; Hydrolase; Nuclease;
Nuclear protein; RNa-binding.
SEQUENCE 245 AA; 26249 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=Fetal brain;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=9606;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              X-linked protein STS1769.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             187:185-191(1997).
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                                                                                            295 AA;
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                                                                                               33582 MW;
                                  11.78;
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Pred. No.
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                                                                                      079BD40D8A56F45E CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   update)
                              DB 1;
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RESULT 15
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                                                                                                                                                                                                                                                                                                                                  King H.W.S., Tempest P.R., Merrifield K.R., Rance A.J.;
"tpr homologues activate met and raf.";
Oncogene 2:617-619(1988).
In FUNCTION: COMPONENT OF THE CYTOPLASMIC FIBRILS OF THE NUCLEAR PORE COMPLEX IMPLICATED IN NUCLEAR PROTEIN IMPORT. ITS AMINO TERMINUS IS INVOLVED IN ACTIVATION OF ONCOGENIC KINASES.
I-SUBCELLULAR LOCATION: CYTOPLASMIC SURFACE OF THE NUCLEAR PORE COMPLEX. THE ASSEMBLY OF THE NPC IS A STEPWISE PROCESS IN WHICH TRP-CONTAINING PERIPHERAL STRUCTURES ASSEMBLE AFTER OTHER COMPONENTS, INCLUDING P62.
I-TISSUE SPECIFICITY: HIGHEST IN TESTIS, LUNG, THYMUS, SPLEEN AND BRAIN, LOWER LEVELS IN HEART, LIVER, AND KIDNEY.

I-I-DISEASE: INVOLVED IN TUMORIGENIC REARRANGEMENTS WITH THE MET, TRK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDLINE-95096166; PubMed-7798308;
Byrd D.A., Sweet D.J., Pante N., Konstantinov K.N., Guan T.,
Saphire A.C.S., Mitchell P.J., Cooper C.S., Aebi U., Gerace L.;
"Tpr, a large coiled coil protein whose amino terminus is involved activation of oncogenic kinases, is localized to the cytoplasmic surface of the nuclear pore complex.";
J. Cell Biol. 127:1515-1526(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TPR_HUMAN P12270;
                                                                                                                                                      entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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01-OCT-1996 (Rel. 34,
16-OCT-2001 (Rel. 40,
Nuclear protein; Transport.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "The human tpr gene encodes a protein of 2094 amino acids that has extensive coiled-coil regions and an acidic C-terminal domain."; oncogene 7:2329-2333(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MEDLINE=93064711; PubMed=1437155; Mitchell P.J., Cooper C.S.;
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                     MIM; 189940; -.
Coiled coil; Proto-oncogene; Chromosomal translocation;
                                                                                       Genew;
                                                                                                                        EMBL; X66397; CAA47021.1; -. EMBL; Y00672; CAA68681.1; -.
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SUMMARIES

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ALIGNMENTS

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SMART; SM00422; HTH_MERR; 1.
PROSITE; PS00552; HTH_MERR_FAMILY; 1.
DNA-binding; Transcription regulation.
SEQUENCE 144 AA; 15652 MW; 1D6E1F50D37A1337
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InterPro; IPR000551; HTH_Mer
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Q52395;
                                                                    "Two aberrant mercury resistance stutzeri plasmid ppB."; Gene 208:37-42(198).
                                                                                                                                                                                                                                                                                                                                                                                                                                           SPECIES-P.Stutzeri; STRAIN-OX; PLASMID-PPB; MEDLINE-86174347; PLAMEd-3007931; Brown N.L., Misra T.K., Winnie J.N., Schmidt A., Selff M., Silver "The nucleotide sequence of the mercuric resistance operons of pla "The nucleotide sequence of the mercuric for mer genes which R100 and transposon Tn501: further evidence for mer genes which enhance the activity of the mercuric ion detoxification system."; Mol. Gen. Genet. 202:143-151(1986).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Mercuric ion-resistance operons of plasmid R100 and transposon the beginning of the operon including the regulatory region and first two structural genes."; Proc. Natl. Acad. Sci. U.S.A. 81:5975-5979(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Greated A., Lambertson L., Williams P.A., Thomas C.M.; "Complete nucleotide sequence of IncP-9 plasmid pWW0."; Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Pseudomonas putida, and
Pseudomonas stutzeri (Pseudomonas perfectomarina).
Pseudomonas stutzeri (Pseudomonas perfectomarina).
Plasmid pWWO, and Plasmid pPB.
Bacteria; Proteobacteria; gamma subdivision; Pseudomonas
                                                                                                                                                                                                                                                           SPECIES=P.stutzeri; STRAIN-OX; PMEDLINE=96105204; PubMed=8529897
                                                                                                                                                                                                                                                                                                                        Kholodii G.Ya, Yurieva O.V., Lomovskaya O.L., Mindlin S.Z., Nikiforov V.G.; "Tn5053, a mercury resistance transposon with J. Mol. Biol. 230:1103-1107(1993).
                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.

SPECIES=P.stutzeri; STRAIN=OX; PI
MEDLINE=93253772; PubMed=8387603;
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MEDLINE=85014891; PubMed=6091128;
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                                                                                                                      Reniero D., Mozzon E., Galli E.,
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                                                                                                                                                                   SEQUENCE FROM N.A.
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                                                                                                                                                                                                               "Cloning and comparison of mercury- and organomercurial-resistance determinants from a Pseudomonas stutzeri plasmid.";
              REGULATORS.
L; AJ344068; CAC86844.1;
L; U90263; AAC38229.1; -.
                                                          SIMILARITY: BELONGS TO THE
                                                                                                                                                                                                 166:77-82(1995).
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TrEMBLrel. 20, Last annotation update)
protein (Organomercurial resistance r
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Shigella flexneri.
Plasmid virulence plasmid pWR501.
Plasmid virulence plasmid pWR501.
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SMART; SM00422; HTH_MERR; 1.

PROSITE; PS00552; HTH_MERR_FAMILY; 1.

Plasmid; DNA-binding; Transcription regulation.

SEQUENCE 144 AA; 15884 MW; F5760BEC88602FC7 CRC64;
                                                                                            01-MAY-2000 (TREMBLIEL 13, 01-MAY-2000 (TREMBLIEL 13, 01-JUN-2001 (TREMBLIEL 17,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRINTS; PR00040; HTHMERR.

SMART; SM00422; HTH_MERR; 1.

PROSITE; PS00552; HTH_MERR_FAMILY; 1.

DNA-binding; Plasmid; Transcription regulation.

DNA-binding; Plasmid; Transcription regulation.

SEQUENCE 172 AA; 18826 MW; 897D139E7BC182A9 CRC64;
                                                   MERR
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Plasmid group 5 plasmid
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Pfam; PF00376; merR; 1.
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                         Pseudomonas putida
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"mer sequences on plasmids.";
"umpr sequences on plasmids.";
"the EMBL/GenBank/DDBJ databases
EMBL; AF092070; AAD52706.1; -.
InterPro; IPR000551; HTH_MerR.
                                                                                                                                                                                                                                                                                                                                                                               Pseudomonas sp. (strain ADP).
Plasmid pMER327, Plasmid RP1, a
Ranteria: Proteobacteria; beta
of Tn5053: a paradigm for a novel family either a mer operon or an integron."; mol. Microbiol. 17:1189-1200(1995).
                                                                                                                                                                                                                    "The sequence of the mer operon of pMER327/419 pMER327/419, 330 and 05."; Gene 146:73-78(1994).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Alcaligenes sp.,
Pseudomonas fluorescens,
                                                                                                                                             SPECIES=C.testosteroni; STRAIN=SE3; Osborn A.M., Bruce K.D., Strike P., Ritchie D.A.; Submitted (DEC-1994) to the EMBL/GenBank/DDBJ dat
                                                                                                                                                                                                                                                                                            SPECIES=Alcaligenes sp., and P.fluorescens; TRANSPOSON=TN5053; MEDLINE=94341572; PubMed=8063107;
                                                                                                                                                                                                                                                                                                                                                                                                                                           unidentified,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pseudomonas.
NCBI_TaxID=303;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
                                                         Nikiforov V.G.;
                                                                        Kholodii G.Y., Mindlin S.Z., Bass I.A.,
                                                                                    MEDLINE=96130850; PubMed=8594337;
                                                                                                   SPECIES=unidentified;
                                                                                                                   SEQUENCE FROM N.A
                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                 Yurieva O.;
                                                                                                                                                                                                                                                                                Hobman J
                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                     NCBI_TaxID=512, 294, 285, 32644, 338,
                                                                                                                                                                                                                                                                                                                                                                      Alcaligenes
                                                                                                                                                                                                                                                                                                                                                                                                                         xanthomonas, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Plasmid.
                                           "Four genes,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           107 SADA 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    47
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               N
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CEEA 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    THCEEASSLAEHKLKDVRERMADLARMEAVLSDLVCACHARKGNVSCPLIASLQGKKEPR 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  THCEEASSLAEHKLKDVREKMADLARMETVLSELVCACHARKGNVSCPLIASLQGSSGTH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SM00422; HTH_MERR; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                               ., Kholodii G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  110
110 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Conservative
                            two ends, and a res region are involved in transpos paradigm for a novel family of transposons carrying
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    110
12211 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                operon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        44.5%;
                                                                                                                                                                                                                                                                                Nikiforov V.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             , Last sequence update)
, Last annotation update)
regulatory protein (MERR protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 273; DB 2
Pred. No. 2e-19;
3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                and Plasmid pADP-1.
a subdivision; Alcal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2C7C09EE8ACB7BCA CRC64;
                                                                                                                                                                                                                                                                                                                                                        47660;
                                                                                                                                                                                                                                                                                Ritchie D.A.,
                                                                        Yurieva O.V., Minakhina S.V.,
                                                                                                                                                                                                                                                                                                                                                                                   Alcaligenaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2; Length 110;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              8;
                                                                                                                                                  databases
                                                                                                                                                                                                                                                     and transposon ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                  Strike P.,
                                              transposition
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
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                                                                                                                                                                                                                                                     of.
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Best Local S
Matches 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      [4]
SEQUENCE FROM N.A.
SPECIES-unidentified;
Kholodii G.Y.;
                                                                                                                                                                                                                                                                                                                                                                                                057492

057492;

01-NOV-1996 (TrEMBLrel. 01,

01-NOV-1996 (TrEMBLrel. 17,

01-JUN-2001 (TrEMBLrel. 17,
  Osborn A.M.;
                                                 SEQUENCE FROM N.A.
                                                                                                Osborn A.M., Bruce K.D., Submitted (DEC-1994) to
                                                                                                                                                      STRAIN-SO1
                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                            MERR.
                                                                                                                                                                                                                                                                                                                                                                              Regulatory protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRINTS; PR00040; HTHMERR.

SMART; SM00422; HTH_MERR; 1.

PROSITE; PS00552; HTH_MERR_FAMILY; 1.

Activator; DNA-binding; Mercuric resistance; Mercury; Plasmid; Repressor; Transcription regulation.

SEQUENCE 144 AA; 16060 MW; E4B3EFEECA317F2D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL;
                                                                                                                                                                                                                                                                                Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                          Enterobacter cloacae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SPECIES-Xanthomonas; PLASMID-RPI; TRANSPOSON-TN5053; MEDLINE-93253772; PubMed-8387603; MEDLINE-93253772; PubMed-8387603; Kholodii G.Ya., Yurieva O.V., Lomovskaya O.L., Gorle Mindlin S.Z., Nikiforov V.G.; "Tn5053, a mercury resistance transposon with integr
                                                                                                                                                                                                                            NCBI_TaxID=550,
                                                                                                                                                                                                                                                                                                     Klebsiella oxytoca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SPECIES-Pseudomonas sp. (strain ADP); STRAIN-ADP; PLASMID-PADP-1 Martinez B.M., Tomkins J., Wackett L.P., Wing R., Sadowsky M.J.; Submitted (JAN-2001) to the EMBL/GenBank/DDBJ databases.
-I- SIMILARITY: BELONGS TO THE MERR FAMILY OF TRANSCRIPTIONAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Russ. J. Genet. 31:1447-1451(1995).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        [nterPro;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  <u>6</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  80
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mol. Biol.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           L; X73112; CAA51538.1; ...
L; L20693; AAB05979.1; ...
L; L23094; CAA80641.1; ...
L; L20694; AAB02644.1; ...
L; L20585; AAB0640.1; ...
L; L40585; AAA98322.1; ...
L; L40585; AAA9832.1; ...
L; L40585; AAA9832.1; ...
L; L40585; AAA9832.1; ...
L; D406917; AAK50289.1; ...
L; D6917; AAK50289.1; ...
DEP00376. MONEY. 1TH_Merr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CEEA 65
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SADA 143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PF00376; merk;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity 82.8
53; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 a mercury resistance transposon Biol. 230:1103-1107(1993).
                                                                                                                                                                                                                               571;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  44.5%;
82.8%;
                                                                                                                                                                                                                                                                                                                               and
                                                                                             the EMBL/GenBank/DDBJ databases.
                                                                                                                       Strike P.,
                                                                                                                                                                                                                                                                              gamma
                                                                                                                                                                                                                                                                                                                                                                                                Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 273; DB Pred. No. 2.7e 3; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ω
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Created)
                                                                                                                                                                                                                                                                           subdivision; Enterobacteriaceae;
                                                                                                                          Ritchie D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   151 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 2; ]
2.7e-19;
hes 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        with integron's ends.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Gorlenko
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 144;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PLASMID-PADP-1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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RESULT 9
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Best Local Similarity
Matches 57; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               007304
007304;
01-JUL-1997
01-NOV-1999
01-JUN-2001
                                                PRINTS; PRO0040; HTHMERR.

MERR; 1.

PROSTTE; PS00552; HTH_MERR_FAMILY; 1.

DNA-binding; Transcription regulation.

DNA-binding; Transcription regulation.
                                                                                                                                                                                                                                                                                                                                                       Yurieva O., Kholodii G., Minakhin L., Go
Mindlin S., Nikiforov V.;
"Intercontinental spread of promiscuous
in environmental bacteria.";
Mol. Microbiol. 24:321-329(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRINTS; PRO0040; HTHMERR.
SMART; SM00422; HTH_MERR; 1.
PROSITE; PSO0552; HTH_MERR_FAMILY; 1.
DNA-binding; Transcription regulation.
SEQUENCE 151 AA; 16559 MW; 238460FCE51754AD CRC64;
                                                                                                                        EMBL; Y09210; CAA70409.2; -.

EMBL; Y18976; CAB81570.1; -.

InterPro; IPB000551; HTH_MerR.

Pfam; PF00376; merR; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EMBL; Z33486; CAA83894.1; ...
EMBL; Z33485; CAA83893.1; ...
InterPro; IPRO00551; HTH_MerR.
Pfam; PF00376; merR; 1.
                                                                                                                                                                                                          Russ.
                                                                                                                                                                                                                                     Kholodii G.Y., Mindlin S.Z.,
Nikiforov V.;
                                                                                                                                                                                                                                                                                        Submitted (JUN-1999) to the
                                                                                                                                                                                                                                                                                                      Kholodii G.;
                                                                                                                                                                                                                                                                                                                   STRAIN=TC97;
                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-TC97
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (MAY-1994)
                                                                                                                                                                                         Russ. J. Genet. 36:365-
                                                                                                                                                                                          "Molecular genetic analysis of the Tn5041 transposition system."; Russ. J. Genet. 36:365-373(2000).
-i-SIMILARITY: BELONGS TO THE MERR FAMILY OF TRANSCRIPTIONAL
                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=97303088; PubMed=9159519;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=306;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Pseudomonas sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MERR protein (Mercuric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (MAY-1994) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     138 L-AASARGSH 146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                62 CEEASSLAEH 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         80 THCEEASGLAEHKLKDVREKMADLARMEAVLSELVCACHARKGNVSCPLIASLQ--DGTK 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 THCEEASSLAEHKLKDVREKMADLARMETVLSELVCACHARKGNVSCPLIASLQGSSGTH 61
                                                                                                                                                                                REGULATORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REGULATORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            l Similarity
57; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Proteobacteria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (TrEMBLrel. 04, Created)
(TrEMBLrel. 12, Last sequence update)
(TrEMBLrel. 17, Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRELIMINARY;
              44.0%;
81.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            44.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 resistance operon regulatory protein).
Score 269.5; DB 2;
Pred. No. 6.2e-19;
1; Mismatches 9;
                                                                                                                                                                                                                                                                                        EMBL/Genßank/DDBJ databases
                                                                                                                                                                                                                                             Gorlenko Z.M., Bass I.A., Kalyaeva E.S.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 269.5; DB 2;
Pred. No. 6.2e-19;
1; Mismatches 9;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     151
                                                                                                                                                                                                                                                                                                                                                                                                             Gorlenko Z., Kalyaeva E.,
                                                                                                                                                                                                                                                                                                                                                                                    mercury-resistance transposons
                            DB 2; Length 151;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        151;
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Conservative

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Q57106;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SPECIES=Acinetobacter sp.; STRAIN=BW3; PLASMID=PKLH207; TRANSPOSON-TNPKLH207 TNPKLH2-LIKE ABERRANT TRANSPOSON; Kholodii G.Z., Yurieva O.V., Mindlin S.Z., Gorlenko Z.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  \begin{tabular}{ll} \beg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRAIN-CH210; TRANSPOSON-TN5059; MEDLINE-97303088; PubMed-9159519; Yurieva O., Kholodii G., Minakhin L., Minakhin C. Niliforov V.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Osborn A.M., Bruce K.D., Strike P., Ritchie D. Submitted (DEC-1994) to the EMBL/GenBank/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Q57106; 008282; 008130; 008287; 008166; 008288; 008185; 01-NOV-1996 [TERMBLEG]. 01, Created)
01-NOV-1996 [TERMBLEG]. 01, Last sequence update)
01-DEC-2001 [TERMBLEG]. 19, Last annotation update)
Regulatory protein (Mercury resistance operon regulatory protein) (MER
                                                                                                                                                                                                                                                                                                                          Gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  dissemination.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nikiforov V.G
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Acinetobacter sp., and Acinetobacter sp. LS56-7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Pantoea agglomerans,
Enterobacter cloacae,
                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=21272500; PubMed=11376944;
                                                                                                                                                                                                                                                                                                                                                                                                                                                      SPECIES=Acinetobacter sp. LS56-7; PLASMID=PKLH204
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mol. Microbiol. 24:321-329(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Alcaligenes sp.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Escherichia coli,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Acinetobacter calcoaceticus,
                                                                                                                                                                                                                                                                                                                                                                            Kholodii G.Y.;
                                                                                                                                                                                                                                                                                                                                                                                                                           TRANSPOSON=TNPKLH204;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "pKLH2-like aberrant transposons and possible mechanisms of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          in environmental bacteria."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NCBI_TaxID=471, 562, 512,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Acinetobacter.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 operon regulatory protein).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   80
                                                                                                                                                                                                                                                                                            SIMILARITY: BELONGS TO THE MERR FAMILY OF TRANSCRIPTIONAL
                                                                                                      709026; CAA70240.1; -... Y08993; CAA70195.1; -... Z33483; CAA83891.1; -... Z33482; CAA83890.1; -... Y08992; CAA70185.1; -... Y09025; CAA70237.1; -...
                                                                                                                                                                                                                                                                      REGULATORS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              shuffling function of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             L-AASARGSH 146
                                                                                                                                                                                                                                                                                                                       269:121-130(2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CEEASSLAEH 71
  PF00376; merR;
                                                    AJ245842; CAC80722.1; -. AJ250860; CAC38823.1; -.
                              IPR000551;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (OCT-1999) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRELIMINARY;
                           HTH_MerR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     549, 550, 472, 107402;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gamma subdivision; Moraxellaceae;
                                                                                                                                                                                                                                                                                                                                                resolvases.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         151 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gorlenko Z., Kalyaeva E.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      D.A.;
BJ databases
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RESULT 12
007300
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Best Local
                                                                                                   01-JUL-1997
01-JUL-1997
01-JUN-2001
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01-MAY-2000
01-JUN-2001
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Q9R9X0;
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SMART; SM00422; HTH_MERR; 1.
PROSITE; PS00552; HTH_MERR_FAMILY; 1.
DNA-binding; Plasmid; Transcription regulation.
DNA-binding; Plasmid; Transcription regulation.
SEQUENCE 151 AA; 16529 MW; 239350FCE51754AD CRC64;
                                                          Pseudomonas sp.,
Pseudomonas sp.
                                                                                                                                   007300;
                                                                                                                                              007300
                                                                                                                                                                                                                                                                                                                                      Bruce K.D., Lilley A.K., Bailey M.J.;
"mer sequences on plasmids.";
Submitted (SEP-1998) to the EMBL/GenBank/DDBJ databases.
EMBL; AF092069; AAD52705.1; -.
InterPro; IPR000551; HTH_MerR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MERR
                                       Plasmid pMR26.
Bacteria; Proteobacteria.
                                                                                  MERR OR MERR1
                                                                                         Mercuric resistance operon
                                                                                                                                                                                                                                                                                                                                                                                                                                            Plasmid group 2 plasmid.
Bacteria; Proteobacteria;
                            NCBI_TaxID=306,
                                                                                                                                                                                                                                                                                    SEQUENCE
                                                                                                                                                                                                                                                                                              NON_TER
                                                                                                                                                                                                                                                                                                                    Plasmid.
                                                                                                                                                                                                                                                                                                                              SMART;
                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=KT2440;
                                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                      Pseudomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pseudomonas putida.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MerR (Fragment).
                                                                                                                                                                                                                                                                                                         NON_TER
                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=303;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              138 L-AASARGSH 146
                                                                                                                                                                                                   57
                                                                                                                                                                                                                                                    Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       08
                                                                                                                                                                                                         2 THCEEASSLAEHKLKDVREKMADLARMETVLSELVCACHARKGNVSCPLIASLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ν
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  THCEEASSLAEHKLKDVREKMADLARMETVLSELVCACHARKGNVSCPLIASLQGSSGTH 61
                                                                                                                                                                                               THCEEASSLAEHKLQDVREKMADLARMETVLSELVCACHARKGNVSCPLIESLQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CEEASSLAEH 71
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       THCEEASGLAEHKLKDVREKMADLARMEAVLSELVCACHARKGNVSCPLIASLQ--DGTK 137
                                                                                                                                                                                                                                                                                                                             SM00422; HTH_MERR; 1.
                                                                                                                                                                                                                                           Similarity
52; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                l Similarity
57; Conserv
                                                                                                                                                                                                                                                                                   111 AA;
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                                                                                                    (TrEMBLrel.
                                                                                                                       (TrEMBLrel.
                                                                                                                                              PRELIMINARY;
                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                             83781;
                                                            ED23-33.
                                                                      and
                                                                                                                                                                                                                                                                                              111
                                                                                                                                                                                                                                                                                   12406 MW;
                                                                                                                                                                                                                                                  43.7%; 96.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          44.0%;
81.4%;
                                                                                                                       04,
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17,
                                                                                                                                                                                                                                                                                                                                                                                                                                              gamma subdivision; Pseudomonadaceae;
                                                                                         regulatory protein (MERR1
                                                                                                                                                                                                                                           ۳.
                                                                                                    Last sequence update)
Last annotation updat
                                                                                                                                                                                                                                                   Score 268; L
                                                                                                                          Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Created)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 269.5; DB 2; Pred. No. 6.2e-19;
                                                                                                                                                                                                                                                                                   642A1FD89A898C97 CRC64;
                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                               144
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                                                                                                                                                                                                                                                              DB
                                                                                                                                                                                                                                                   .3e-19;
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                                                                                                                                                                                                                                                             Length 111;
                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length
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                                                                                          protein).
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                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2,
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SPECIES=Pseudomonas sp.; STRAIN=K-62; PLASMID=PMR26;

SEQUENCE FROM N.A

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RESULT 13
P77071
P77077
DT 01-FE
ON MEDR
OC Bacte
OC Bacte
OC Bacte
OC NCBL
OC BACTE
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SPECIES-Pseudomonas sp. ED23-33; TRANSPOSON-TN5058; Minakhina S., Minakhin L., Kholodii G., Mindlin S., Gorlenko Z.H. Yurieva O., Nikiforov V.; "Molecular inventory of transposons from environmental bacteria: epidemic dissemination of Tn21-, Tn5041-, and Tn5053-related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=97311403; PubMed=9168120;
Kiyono M., Omura T., Inuzuka M., Fujimori H., Pan-Hou H.;
Kiyono tide sequence and expression of the organomercurial-resistance
determinants from a Pseudomonas K-62 plasmid pMR26.";
Gene 189:151-157(1997).
                                                                                                                                                                                                                            MEDLINE=85155497; PubMed=6099319; Ogawa H.I., Tolle C.L., Summers A "Physical and genetic map of the inorganic mercury resistance (Hyr Gene 32:311-320(1984).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P77071; Q91UN8;
01-FEB-1997 (TrEMBLrel. 02, Created)
01-FEB-1997 (TrEMBLrel. 02, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRINTS; PRO0040; HTHMERR.
SMART; SM00422; HTH_MERR; 1.
PROSITE; PS00552; HTH_MERR_FAMILY; 1.
DNA-binding; Plasmid; Transcription regulation.
SEQUENCE 144 AA; 15651 MW; AE25F7DF733A6734 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; D83080; BAA20334.1; -.
EMBL; Y17897; CAC14697.1; -.
InterPro; IPR000551; HTH_Merr.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pseudomonas sp. ED23-33, and Rhizobium meliloti) Plasmid R831b, Plasmid pMR26, and Plasmid ps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Merr protein (MERR2 protein).
MERR OR MERR2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Liebert C.A., Watson
                               SPECIES-E.coli;
                                                      SEQUENCE FROM N.A.
                                                                                                       Submitted (DEC-1996)
                                                                                                                                                      SPECIES=E.coli;
                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=562,
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Escherichia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Proteobacteria; gamma subdivision;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pseudomonas sp. K-62,
Pseudomonas sp. ED23-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Escherichia coli,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       P77071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pfam; PF00376; merR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           transposons."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LAGAST 143
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           54;
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                                                                                                                                 Totis P.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                   76885,
                                                                                                                                 Summers
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A.L.,
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                                                                                                       the
                                                                                                                                                                                                                                                                                                         Summers A.O.;
     Summers A.O.;
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                                                                                                                                 A.O.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Score 268; DB
Pred. No. 8.2e
5; Mismatches
                                                                                                       EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                      the organomercury resistance (Omr) (Hgr) loci of the IncM plasmid R83
                                                                                                                                                                                                                                                                                                                                                                                                                                   382;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       144 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 2; Length 144; .2e-19;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         pSB102
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
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                                                                                                                                                                                                                                                        Omr) and
R831b.",
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2
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RESULT 14
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM NO...

SPECIES-R. Roelilotti, PLASMID-PSB102;

TRANSPOSON-MERCURY RESISTANCE TRANSPOSON TN5718;

TRANSPOSON-MERCURY RESISTANCE TRANSPOSON TN5718;

Transposon-Mercury Resistance Transposon Tn5718;
                                                                                                                                                                                   Q44191 PRELIMINARY;
Q44191;
Q1-NOV-1996 (TrEMBLrel. 01,
Q1-NOV-1996 (TrEMBLrel. 01,
Q1-DEC-2001 (TrEMBLrel. 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            mercury resistance plasmid pSB102 isolated from a microbial porcesiding in the rhizosphere of alfalfa."; submitted (DEC-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SPECIES-Pseudomonas sp. Minakhina S., Minakhin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Nucleotide sequence of the two mer operons from a Peudomonas K-62 plasmid pMR26.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SPECIES-Pseudomonas sp. Kiyono M., Hou H.P.;
                            Osborn A.M., Bruce K.D., Strike P., Ritchie D.A.;
                                            STRAIN-T217;
                                                                                                                      Bacteria; Proteobacteria;
                                                                                                                                        Agrobacterium tumefaciens.
                                                                                                                                                                     Regulatory protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           prosite; ps00552; HTH_MERR_FAMILY; 1.
DNA-binding; Plasmid; Transcription regulation.
sequence 144 AA; 15623 MW; 9DF4ED0B8A57D75D CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRINTS; PR00040; HTHMERR. SMART; SM00422; HTH_MERR; 1.
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Pfam; PF00376; merR; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AB013925; BAA36431.1; EMBL; X17897; CAC14703.1; -. EMBL; AJ304453; CAC79199.1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EMBL; U77087;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (AUG-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               epidemic dissemination of Tn21-,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
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from Mercury Polluted and Pristine Environments.";
                                                           SEQUENCE FROM N.A.
                                                                                        NCBI_TaxID=358;
                                                                                                           Rhizobiaceae;
                                                                                                                                                        MERR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Selbitschka W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The genetic organization and evolution of the broad-host-range mercury resistance plasmid pSB102 isolated from a microbial popu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Molecular inventory of transposons from environmental bacteria: pidemic dissemination of Tn21-, Tn5041-, and Tn5053-related
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Turieva O., Nikiforov V.;
                Sequence Conservation between Regulatory Mercury Resistance Genes
                                                                                                                                                                                                                                                                                                                             138
                                                                                                                                                                                                                                                                                                                                                        62 CEEASS 67
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REGULATORS
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                                                                                                                                                                                                                                                                                                                                                                                     THCEEASSLAEHKLQDVREKMADLARMEAVLSDLVCACHSRQGNVSCPLIASLQG--GTS 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                  54;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                           Rhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB49638.1;
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81.8%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ED23-33; TRANSPOSON=TN5058; L., Kholodii G., Mindlin S.,
                                                                                                                         alpha subdivision; Rhizobiaceae group;
                                                                                                                                                                                     Last sequence update)
Last annotation updat
                                                                                                                                                                                                                   Created)
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Pred. No. 8.2e-19;
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                                                                                                                                                                                                                                                   151 AA
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RESULT 15
Q99093
ID Q9909
AC Q9909
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                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
SPECIES-A.lwoffii; PLASMID-PKLH103, PKLH102, AND PKLH104;
Kholodii G.Y., Mindlin S.Z., Lomovskaya O.L., Gorlenko Z.M.,
Yurieva O.V., Nikiforov V.G.;
"PKLH1-like aberrant mercury resistance transposons of environmental Acinetobacter strains: spread, polymorphism and possible origin.";
Submitted (DEC-1999) to the EMBL/GenBank/DDBJ databases.
                     "The shuffling function of resolvases.";
Gene 269:121-130(2001).
-I- SIMILARITY: BELONGS TO THE MERR FAMILY OF TRANSCRIPTIONAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   099093

099093; PRELIMINARY; PRT; 151 AA.

099093; O1-NOV-1996 (TrEMBLrel. 01, Created)

01-NOV-1996 (TrEMBLrel. 01, Last sequence update)

01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
                                                                                                                                           SPECIES-Acinetobacter sp.; STRAIN=ED45-25; PLASMID=PKLH205; MEDLINE=21272500; PubMed=11376944;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kholodii G.Y., Lomovskaya O.L., Gorlenko Z.M., Mindlin S.Z., Yurieva O.V., Nikiforov V.G.;
"Molecular characterization of an aberrant mercury resistance transposable element from an environmental Acinetobacter strain.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SPECIES-A.calcoaceticus; PLASMID-PKLH2; MEDLINE-94134837; PubMed-8302940;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SPECIES=A.calcoaceticus; PLASMID=PKLH2; Lomovskaya O.L., Nikiforov V.G.; Genetika 24:1064-1071(1988).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRINTS; PR00040; HTHMERR.
SMART; SM00422; HTH_MERR; 1.
PROSITE; PS00552; HTH_MERR_FAMILY; 1.
DNA-binding; Transcription regulation.
SEQUENCE 151 AA; 16591 MW; 548460FCE50240FC CRC64;
                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Plasmid 30:303-308(1993).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mer operon regulatory protein.
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Pfam; PF00376; merr; 1.
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      REGULATORS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Plasmid pKLH103, Plasmid pKLH102, Plasmid pKLH104, and
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Pred. No. 1.2e-18;
2; Mismatches 9;
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             Search completed: May 28,
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Best Local
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EMBL; AJZ51539; CAB65953.1; -
EMBL; AJZ51517; CAB65939.1; -
EMBL; AJZ51009; CAB65945.1; -
EMBL; AJZ51009; CAB65949.1; -
EMBL; AJZ51706; CAC39408.1; -
InterPro; IPRO00551; HTH_Merr.
Pfam; PF00376; merr; 1.
time : 34 secs
                                                                                                                                                                                                                     PRINTS; PRO0040; HTHMERR.
SMART; SM00422; HTH_MERR; 1.
PROSITE; PS00552; HTH_MERR_FAMILY; 1.
DNA-binding; Plasmid; Transcription regulation.
DNA-binding; Plasmid; Transcription regulation.
SEQUENCE 151 AA; 16561 MW; 549350FCE50240FC CRC64;
                                                         138 L-AASARGSH 146
                                                                                                            62 CEEASSLAEH 71
                                                                                                                                                                      Local Similarity es 56; Conserv
                                                                                                                         2 THCEEASSLAEHKLKDVREKMADLARMETVLSELVCACHARKGNVSCPLIASLQGSSGTH 61
                                                                                                                                                                      Conservative
                                                                                                                                                                                  43.5%;
80.0%;
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Pred. No. 1.2e-18;
2; Mismatches 9;
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Maximum DB
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1: /cgn2_6/ptodata/1,
2: /cgn2_6/ptodata/1,
3: /cgn2_6/ptodata/1,
4: /cgn2_6/ptodata/1,
5: /cgn2_6/ptodata/1,
6: /cgn2_6/ptodata/1,
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Match
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/cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
/cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
/cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
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 US-09-134-001C-2982
US-09-188-930-332
US-09-188-930-192
US-08-685-576-4
US-09-095-443-2
US-08-369-796-12
US-08-416-581B-1
US-08-416-581B-9
US-08-852-091-12
US-08-852-091-12
US-08-956-652-12
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US-08-013-710-9
US-08-08-710-09-14
US-08-015-676-11
US-08-016-676B-1
                                                                                                                                                                                                                                                                                                                                                                                                           SUMMARIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (without alignments)
229.499 Million cell updates/sec
Sequence 2982, Ap
Sequence 332, App
Sequence 192, Appli
Sequence 2, Appli
Sequence 12, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 12, Appli
Sequence 13, Appli
Sequence 6, Appli
Sequence 6, Appli
Sequence 6, Appli
Sequence 14, Appli
Sequence 17, Appli
Sequence 18, Appli
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Sequence 11, Appli
Sequence 12, Appli
Sequence 12, Appli
Sequence 12, Appli
Sequence 14, Appli
Sequence 14, Appli
Sequence 17, Appli
Sequence 17, Appli
Sequence 18, Appli
Sequence 19, Appli
Sequence 11, Appli
                                                                                                                                                                                                                                                                                                                                                                    Description
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RESULT 2 US-09-188-930-332 US-09-188-930-332 ; Sequence 332, Application US/09188930A ; Patent No. 6150502 ; GENERAL INFORMATION: ; APPLICANT: Watson, James D. ; APPLICANT: Strachan, Lorna ; APPLICANT: Steeman, Matthew ; APPLICANT: Oncust, Rene ; APPLICANT: Oncust, Rene ; APPLICANT: Murison, James Greg	50LIASLQGSSGTHCEEASSLAEHKLKDVREKMADLARMETVLSELVCACHARKGN 1	Query Match 15.0%; Score 92; DB 4; Length 138; Best Local Similarity 21.8%; Pred. No. 0.0036; Matches 27; Conservative 16; Mismatches 37; Indels 44; Gaps Qy 28 METVLSELVCAC	ACID SEQUENCES RELATING TO STICS AND THERAPEUTICS	28 68.5 11.2 955 2 US-08-428-414A-3 Sequence 3, App 29 68.5 11.2 955 5 PCT-US94-00324-1 30 68 11.1 1886 4 US-08-938-105-3 31 66.5 10.8 425 3 US-09-020-684-5 32 66.5 10.8 425 3 US-09-020-685-5 34 66.5 10.8 425 3 US-09-020-685-5 36 66.5 10.8 425 4 US-09-020-685-5 36 66.5 10.8 574 1 US-08-049-473-2 37 66.5 10.8 574 1 US-08-049-473-2 38 66.5 10.8 574 1 US-08-049-473-2 39 66.5 10.8 577 4 US-08-312-648-2 39 66.5 10.8 577 4 US-08-312-648-2 39 66.5 10.8 577 4 US-08-313-648-2 39 66.5 10.8 577 4 US-08-393-038-7 40 66.5 10.8 577 4 US-08-393-038-7 41 66.5 10.8 783 1 US-08-539-3038-7 42 65.5 10.7 386 2 US-08-559-3038-7 43 65.5 10.7 386 4 US-09-775-828-75 44 65.5 10.7 859 3 US-08-775-828-75 39 Sequence 75, Ap 45 65.5 10.7 810 2 US-08-320-170A-34 ALIGNMENTS ALIGNMENTS
		2;	STAPHYLOCOCC	Appli Appli

TITLE OF INVENTION: Compositions Isolated From Skin Cells

APPLICANT:

Nakano, Takeshi

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RESULT 4
US-08-685-576-4
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; LOCATION: (239)...(239)
US-09-188-930-192
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                                              Sequence 4, Applic Patent No. 5906819
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/188,930A CURRENT FILING DATE: 1998-11-09 NUMBER OF SEQ ID NOS: 348 SOFTWARE: FASTSEQ for Windows Version 3.0 SEQ ID NO 332 LENGTH: 299 TYPE: PRT ORGANISM: Mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
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                                                                                                                                                                                                                                                                                                       Query Match
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SOFTWARE: FastSEQ for
SEQ ID NO 192
LENGTH: 299
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Watson, James D.
APPLICANT: Strachan, Lorna
APPLICANT: Strachan, Matthew
APPLICANT: Orrust, Rene
APPLICANT: Murison, James Greg
TITLE OF INVENTION: Compositions Isolated From Skin Cells
TITLE OF INVENTION: and Methods For Their Use
FILE REFERENCE: 11000.1011c1
CURRENT APPLICATION NUMBER: US/09/188,930A
CURRENT FILING DATE: 1998-11-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                               GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                 NAME/KEY: UNSURE LOCATION: (98)...(98)
                                                                                                                                                                                                                                                                                                                                                                                                                       FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: mouse
                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
 APPLICANT:
                APPLICANT:
                                                                                                                                                 97
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                                                                                                                                                                                                                                                                                     Match 12.7%;
Local Similarity 24.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         77 --- CACRNGGLCHATNGSCSCPLGWMGPHCE 104
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     92 ELVCA-----CHARKGNVSCPSAWSHPQFE 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     38 ACHARKGNVSCPLIASLQGSSGTHCEEA-----SSLAEHKLKDVREKMADLARMETVLS 91
                                                                                                                                                                          IASLQGSSGTHCEEASSLAEHKLKDVREKMADLARMETVLSELVCACHARKGNVSC 106
                                                                                                                                                                                                             HCERGCPQDRFGKGCEHK-
                                                                                                                                                                                                                                           HCEEA-----CHARKGNVSCPL 50
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o. 6150502
                                                             Application US/08685576
                                                                                                                                              -GXMGPHCEHACPAGRYGAACLLE--
Kaibuchi,
Iwamatsu,
                                                                                                                                                                                                                                                                           Conservative
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Akihiro
                                                                                                                                                                                                                                                                      Score 78; DB of Pred. No. 0.38
5; Mismatches
                                                                                                                                                                                                                                                                           5;
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                                                                                                                                                                                                                                                                                                       DB 4; Length 299,
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                                                                                                                                              --CSC---QNNGSC 128
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GENERAL INFORMATION:

APPLICANT: Plowman, Gre

Gregory

TITLE OF INVENTION: DIAGNOSIS AND TREATMENT TITLE OF INVENTION: OF ALP RELATED DISORDER

CORRESPONDENCE ADDRESS

STREET: STREET: ADDRESSEE:

E: Lyon & Lyon 633 West Fifth Street Suite 4700

NUMBER OF SEQUENCES:

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                                 US-09-095-443-2
                                                     RESULT 5
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Patent No. 6342593
                Sequence
                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                   Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME: Bent, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 168
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)672-5300
TELEPAX: (202)672-5399
                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 1388 amino aci
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 8-
FILING DATE: 05-JAN-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 20007-5109
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                          MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 7-325129
FILING DATE: 20-NOV-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Takahashi, No. 5906819uaki
TITLE OF INVENTION: RHO TARGET PROTEIN RHO-KINASE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT:
                                                                                                         947 ELEIKEMMARHKQELTEKDATIASLEETNRTLTSDVANLANEKEELNNKLKDVQEQLSRL 1006
                                                                                                                                                                              887 CEEKTKLGKELQQKKQELQDERDSLAAQLEITLTKADSEQLARSIAEEQYSDLEKEKIMK 946
                                                                                                                                           34
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
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                                                                                                                                                                                                                                                                    Local Similarity
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                                                                                                                                                                                                                 4 CEEASSIA------HKLKDVREKMA-------DLAR------METVLS 33
                                                                                                                                           EL----VCACHARKGNVSCPLIASLQGSSGTHCEEASSLA----EHKLKDVREKMADL 83
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20007-5109
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                                                                                                                                                                                                                                                                                                                                                                          amino acid
              Application US/09095443
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                                                                                                                                                                                                                                                                                                                                                                                            1388 amino acids
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                                                                                                                                                                                                                                                   Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              26-APR-1996
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                                                                                                                                                                                                                                                                  Score 72; DB
Pred. No. 13;
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                                                                                                                                                                                                                                                 Mismatches
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                                                                                                                                                                                                                                                                                    DB 2; Length 1388;
                                                                                                                                                                                                                                                   Indels
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COUNTRY:

Los Angeles

California

U.S.A

90071-2066

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
TELEPHONE: (213) 489-1600
TELEFAX: (213) 955-0440
TELEX: 67-3510
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1274 amino acids
                                                                                                                                                                                                                                                                                                                                                                          Sequence 12, Application US/08369796 Patent No. 5716622
                                                              APPLICANT: James L. .....
APPLICANT: Zilong Wen
APPLICANT: Zilong Wen
APPLICANT: Curt M. Horvath
APPLICANT: Chong Zhong
TITLE OF INVENTION: FUNCTIONALLY ACTIVE REGIONS OF SIGNAL
TITLE OF INVENTION: TRANSDUCER AND ACTIVATOR OF TRANSCRIPTION (STAT) PROTEINS
NUMBER OF SEQUENCES: 39
CORRESPONDENCE ADDRESS:
ANDRESSEE: Klauber & Jackson
ANDRESSEE: Klauber & Jackson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: James E. Darnell, Jr.
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: FASTSEV LL.
CURRENT APPLICATION DATA:
CURRENT APPLICATION NUMBER: US/09/095,443
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: 60/0 FILING DATE: June 12, 19 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: storage
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  116 GOAGAISITS 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           99 ARKGNVSCPS 108
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 39 CHARKGNVSCPLIASLQGSSGTHCEEASSLAEHKLKDVREKMADLARMETVLSELVCACH 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity les 32; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           REGISTRATION NUMBER: 32,327
REFERENCE/DOCKET NUMBER: 235/055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NAME: Warburg, Richard J. REGISTRATION NUMBER: 32,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM: IBM P.C. DOS 5.0 SOFTWARE: FastSEQ for Windows 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5 EASSLYSEEKAKLLREMMAKIEDKNEVLDQFMDSMQLDPETVDNLDAYSHIPPQLMEKCA 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         18; Mismatches 44; Indels 36;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1, Application US/08416581B Patent No. 5719042 GENERAL INFORMATION:
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                                                                           FILING DATE: 04-APR-1994
ATTORNEY/AGENT INFORMATION:
NAME: Nakamura, Dean H.
REGISTRATION NUMBER: 33,981
REFERENCE/DOCKET NUMBER: Q-37
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)293-7060
                                           INFORMATION FOR SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 201 343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
                         SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                   SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                     CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Kishimoto, Tac
APPLICANT: Akira, Shizuo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: TRANSCRIPTION FACTOR APRENUMBER OF SEQUENCES: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: protein
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NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/369,796
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                                                                                                                                                                                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                   APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Washington
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          5 EEASSLAEHKLKDVR-----EKMADLARMETVLSELVCACHARKGN-VSCPLIASLQ 55
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2100 Pennsylvania Avenue,
770 amino acids
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                                       (202)293-7860
OR SEQ ID NO: 1:
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                                                                                                                       Q-37891
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TYPE:

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US-08-416-581B-5
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                                                                                                                                                          Matches
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Best Local Similarity
                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 770 amino acids
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 6-65825/1994
APPLICATION NUMBER: 04-APR-1994
APPLICATION DATE: 04-APR-1994
                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: Q-
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202)293-7060
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CORRESPONDENCE ADDRESS:
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APPLICANT: Akira, Shizuo
                                                                                                                                                                                                                                                        TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Nakamura, Dean H.
REGISTRATION NUMBER: 33,981
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   126 GGQANHPTAAVVTEKQQMLEQHLQDVRKRVQDLEQKMKVVENL 168
126 GGQANHPTAAVVTEKQQMLEQHLQDVRKRVQDLEQKMKVVENL 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              73 QESNVLYQHNLRRIKQFLQSRYLEKPMEIAR-----IVARCLWEESRLLQTAATAAQQ 125
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
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                                        56 GSSGTH-----CEEASSLAEHKLKDVREKMADLARMETVLSEL 93
                                                                             73 QESNVLYQHNLRRIKQFLQSRYLEKPMEIAR-----IVARCLWEESRLLQTAATAAQQ 125
                                                                                                                                                                                                                                                                                                 TYPE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Match 11.5%; Score 70.5; DB 1; Length 770; Occal Similarity 23.3%; Pred. No. 9.2;
                                                                                                                    5 EEASSLAEHKLKDVR-----EKMADLARMETVLSELVCACHARKGN-VSCPLIASLQ 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24; Conservative
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                                                                                                                                                                                                                                                                                               amino acid
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                                                                                                                                                            Conservative
                                                                                                                                                                                                                                                                                                                                                                            (202)293-7860
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Floppy disk
                                                                                                                                                                             11.5%; Score 70.5; DB 1; Length 770; 23.3%; Pred. No. 9.2;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                US/08/416,581B
                                                                                                                                                          20; Mismatches
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                                                                                                                                                            38; Indels
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RESULT 9
US-08-416-581B-9
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                            Patent No. 5883228
                                                                                                                                                                                                                                               Sequence 12,
                                                                                                                                                                                                         GENERAL INFORMATION:
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INFORMATION FOR SEQ ID NO:
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APPLICANT: Akira, Shizuo
TITLE OF INVENTION: TRANSCRIPTION FACTOR APRE
NUMBER OF SEQUENCES: 11

CORRESPONDENCE ADDRESS:
ADDRESSEE: SUGHRUE, MION, ZINN, MACPEAK & SEAS
STREET: 2100 Pennsylvania Avenue, N.W.
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/416,581B
FILING DATE: 04-APR-1995
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REFERENCE/DOCKET NUMBER: Q-
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: JP 6-65825/1994 FILING DATE: 04-APR-1994 ATTORNEY/AGENT INFORMATION: NAME: NAKE: NAKENULA, Dean H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                       TITLE OF INVENTION: FUNCTIONALLY ACTIVE REGIONS OF SIGNAL TITLE OF INVENTION: TRANSDUCER AND ACTIVATOR OF TRANSCRIPTION (STAT) PROTEINS NUMBER OF SEQUENCES: 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
                                                                                                                                                            APPLICANT: James E. Darnell, Jr. APPLICANT: Zilong Wen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein
                                      CORRESPONDENCE ADDRESS:
                                                                                                                     APPLICANT: Curt M. Hory APPLICANT: Zhong Zhong
                                                                                                                                                                                                                                                                                                                                                  126 GGQANHPTAAVVTEKQQMLEQHLQDVRKRVQDLEQKMKVVENL 168
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TELEFAX: (202)293-7860
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  STREET:
                   ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH:
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411 Hackensack Avenue
                                                                                                                                           Zilong Wen
Curt M. Horvath
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                     Klauber & Jackson
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CITY: Hackensack

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Patent No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: 12:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/820,754
FILING DATE: 19-MAR-1997
                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: RECEPTOR RECOGNITION FACTORS, PROTEITITLE OF INVENTION: SEQUENCES AND METHODS OF USE THEREOF NUMBER OF SEQUENCES: 25
                                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-116
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
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ATTORNEY/AGENT INFORMATION:
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PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             126 GGQANHPTAAVVTEKQQMLEQHLQDVRKRVQDLEQKMKVVENL 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 133521
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                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                               CITY: Hackensack
                                                                                                                                                                                                                                                  STREET:
                                                                                                                                                                                                                                                                     ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  56 GSSGTH-----CEEASSLAEHKLKDVREKMADLARMETVLSEL 93
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TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: FILING DATE: 06-MA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           5 EEASSLAEHKLKDVR------EKMADLARMETVLSELVCACHARKGN-VSCPLIASLQ 55
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Jackson Esq., David A. REGISTRATION NUMBER: 26,742
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                          New Jersey
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                                                                                                                                                                                                                                         411 Hackensack Avenue
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                                                                                                                                                                                       USA
                                                                                                                                                                                                                                                                                                                                                                                                          Darnell Jr., James E. Schindler, Christian W. Fu, Xian-Yuan
                                                                                                                                                                                                                                                                                                                                                                                       Wen, Zilong
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06-JAN-1995
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                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                      APPLICANT: Zhong, Zhong
TITLE OF INVENTION: RECEPTOR RECOGNITION FACTORS, PROTEIN
TITLE OF INVENTION: SEQUENCES AND METHODS OF USE THEREOF
NUMBER OF SEQUENCES: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
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APPLICANT:
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TELEPHONE: 201 487-5800
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ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esg., David A.
REGISTRATION NUMBER: 26,742
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    126 GGQANHPTAAVVTEKQQMLEQHLQDVRKRVQDLEQKMKVVENL 168
CLASSIFICATION:
                    FILING DATE:
                                    APPLICATION NUMBER:
                                                                                                                                                                                                      STATE:
                                                                                                                                                                                                                       CITY: Hackensack
                                                                                                                                                                                                                                    STREET:
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APPLICATION NUMBER: US 07/980,498
                                                                                                                                                                                   COUNTRY:
                                                                                                                                                                                                                                                       ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US 07/854,296 FILING DATE: 19-MAR-1992
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                                                                                                                                                                                                  New Jersey
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411 Hackensack Avenue
                                                                                                                                                                                   USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           11.5%; Score 70.5; DB 2; Length 770; 23.3%; Pred. No. 9.2; tive 20; Mismatches 38; Indels 2
                                    US/08/956,652
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APPLICATION NUMBER: 0

APPLICATION NUMBER:

11-MAR-1994

US 07/980,498

US 08/212,185

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Best Local Similarity
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LENGTH: 770 amino acid
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REGISTRATION NUMBER: 26.742
REFERENCE/DOCKET NUMBER: 600-1-073 CIP
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
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APPLICATION NUMBER: US 0:
FILING DATE: 19-MAR-1992
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APPLICATION NUMBER: US 0
FILING DATE: 24-SEP-1993
                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                            APPLICANT: Zhong, Zhong
TITLE OF INVENTION: RECEPTOR RECOGNITION FACTORS, PROTEIN
TITLE OF INVENTION: SEQUENCES AND METHODS OF USE THEREOF
NUMBER OF SEQUENCES: 25
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NAME: Jackson Esq., David
                                                       CURRENT APPLICATION DATA: APPLICATION NUMBER: US
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PRIOR APPLICATION DATA:
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                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TOPOLOGY:
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                   CLASSIFICATION:
                                       FILING DATE:
                                                                                                                                                                                               COUNTRY: UZIP: 07601
                                                                                                                                                                                                                                                  CITY: Hackensack
                                                                                                                                                                                                                                                                                          ADDRESSEE:
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amino acid
                                                                                                                                                                                                                                 New Jersey
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                                                                                                                                                                                                                                                                      411 Hackensack Avenue
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Schindler, Christian W.
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                                                                                                                                                                                                                                                                                                                                                                                                                            Fu, Xian-Yuan
                                                                                                                                                                                                                 USA
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                                                                                                                                                     Floppy disk
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23.3%;
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                                                           us/08/956,869
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Pred. No. 9.2;
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APPLICANT:
APPLICANT:
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PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO US93/02569
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILING DATE: 24-SEP-1993
ATTORNEY/AGENT INFORMATION:
NAME: Jackson ESG., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600
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LENGTH: 770 amino aci
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                                                    CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., Davi
                                                                                                                                           COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTTWARE: Patentin Release #1.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                             TITLE OF INVENTION: A CRYSTAL OF THE N-TERMINAL DOMAIN OF A TITLE OF INVENTION: STAT PROTEIN AND METHODS OF USE THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEFAX: 201
TELEFAX: 133521
NAME: Jackson Esq., David A. REGISTRATION NUMBER: 26,742
REFERRICE/DOCKET NUMBER: 600
FELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               126 GGQANHPTAAVVTEKQQMLEQHLQDVRKRVQDLEQKMKVVENL 168
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                                                                                                                            APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                            ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         24; Conservative
                                                                                                                                                                                                                                                       07601
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                                                                                                                                                                                                                                                                                                                        411 Hackensack Avenue, 4th Floor
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24-SEP-1993
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                                                                                                                                                            Release #1.0, Version #1.30
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                                                                                                                            US/09/012,710
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                    600-1-194
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US-08-948-547-12
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                                                                                                                                                                                                              CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/212,185
FILLING DATE: 11-MAR-1994
APPLICATION NUMBER: US 07/980,498
FILLING DATE: 23-NOV-1992
PRIOR APPLICATION DATA:
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INFORMATION FOR SEQ ID NO:
           APPLICATION NUMBER: US 08/126
FILING DATE: 24-SEP-1993
ATTORNEY_AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
                                                                                                                                                               FILING DATE: 19-MAR-PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                     MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Zhong, Zhong
TITLE OF INVENTION: RECEPTOR RECOGNITION FACTORS, PROTEIN
TITLE OF INVENTION: SEQUENCES AND METHODS OF USE THEREOF
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
                                                                                                           PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
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HYPOTHETICAL:
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                                                                                                                              APPLICATION NUMBER: FILING DATE: 19-MAF
                                                                                                                                                                                   APPLICATION NUMBER: US 07/854,296 FILING DATE: 19-MAR-1992
                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/948,547 FILING DATE:
 REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: Hackensack
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STRANDEDNESS: sin
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al Similarity 23.3%; Pred. No. 9.2;
24; Conservative 20; Mismatches 38; Indels 21; Gaps
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600-1-073 CIP
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION: TELEPHONE: 201 487-5800
                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS
126 GGQANHPTAAVVTEKQQMLEQHLQDVRKRVQDLEQKMKVVENL 168
                                      56 GSSGTH-----CEEASSLAEHKLKDVREKMADLARMETVLSEL 93
                                                                       73 QESNVLYQHNLRRIKQFLQSRYLEKPMEIAR-----IVARCLWEESRLLQTAATAAQQ 125
                                                                                                                                                                                                                                                                            LENGTH: 770 amino acids TYPE: amino acid TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: 201 343-1684
                                                                                                                                                    Local Similarity 23.3%; Pred. No. 9.2; nes 24; Conservative 20; Mismatches
                                                                                                             5 EEASSLAEHKLKDVR------EKMADLARMETVLSELVCACHARKGN-VSCPLIASIQ 55
                                                                                                                                                                        11.5%; Score 70.5; DB 3; Length 770; 23.3%; Pred. No. 9.2;
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Search completed: May 28, 2003, 10:29:38
Job time: 18 secs

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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Perfect score:
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'(cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
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'(cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
'(cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
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'(cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:*
'(cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:*
'(cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:*
'(cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
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                 296
299
299
337
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                 US-10-082-830-260

US-09-796-753-116

US-10-045-792-8

US-10-038-010-56

US-09-925-302-780
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US-09-866-050A-332
US-09-866-050A-332
US-10-259-042-22
US-10-259-042-22
US-10-084-94-11
US-09-884-001-19
US-09-988-275-7
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207.200 Million cell updates/sec
Sequence 2, Appli
Sequence 12, Appl
Sequence 10, Appli
Sequence 7, Appli
Sequence 7, Appli
Sequence 116, Appli
Sequence 8, Appli
Sequence 56, Appl
Sequence 780, App
Sequence 24, Appl
Sequence 24, Appl
                                                                                                                                                                                                                                                                                                                                            Sequence 458, App
Sequence 192, App
Sequence 332, Appl
Sequence 22, Appl
Sequence 34088, A
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                                                                                                                                                                                                                                                                                                Sequence 11, Appl
Sequence 19, Appl
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10.4	10.4	10.4	10.4	10.4	10.4	10.4	10.4	10.4	10.4	10.4	10.4	10.4	10.4	10.4	10.4	10.5	10.7	10.7	10.7	10.8	10.8	10.8	11.3	11.3	11.3
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US-10-092-390-2	US-10-028-392-5	US-09-796-753-124	US-09-796-753-100	US-10-092-390-4	US-09-866-050A-335	US-09-764-869-917	US-10-091-504-917	US-10-116-260-1	10-1	US-10-115-671-1	US-10-116-561-1	US-10-115-695-1	US-09-254-590-1	US-09-922-364A-1	US-09-738-626-5780	US-09-381-624A-3	US-10-011-064-5	US-09-976-165-34	US-09-753-143-75	US-09-842-758-18	US-09-864-761-44770	US-10-072-841-29	US-10-043-487-330	ω	US-09-800-362-2
Sequence 2, Appli	Sequence 5, Appli		100	4 . A	35		917.	_ [- !	Sequence 1. Appli	- !	1	۲.		5780, Ap	ω	5 A	34,	75.			29,	30	e 13	Sequence 2, Appli

ALIGNMENTS

RESULT 1 US-09-866-050A-458 Sequence 458, Application US/09 Sequence 158, Discourage VS/09 Publication No. US20030040471A1

Application US/09866050A

GENERAL INFORMATION:

APPLICANT: Watson, James D.
APPLICANT: Strachan, Lorna
APPLICANT: Sleeman, Matthew
APPLICANT: Sleeman, Matthew
APPLICANT: Murison, James G.
APPLICANT: Kumble, Krishanand D.
TITLE OF INVENTION: Compositions Isolated From Skin Cells
TITLE OF INVENTION: and Methods for Their Use
FILE REFERENCE: 11000.1011c4U
CURRENT APPLICATION NUMBER: US/09/866,050A

NUMBER OF SEQ ID NOS: 725
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 458
LENGTH: 296

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US-09-866-050A-192
; Sequence 192, Application US/09866050A
; Publication No. US20030040471A1
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                         TYPE: PRT
ORGANISM: Mouse
                                                                                                      74 --- CACRNGGLCHATNGSCSCPLGWMGPHCE 101
                                                                                                                                      92 ELVCA-----CHARKGNVSCPSAWSHPQFE 116
                                                                                                                                                                 38 ACDPVSGTCICP----PGKTGGHCERGCPQDRFGKGCEHK--
                                                                                                                                                                                                38 ACHARKGNVSCPLIASLQGSSGTHCEEA-----SSLAEHKLKDVREKMADLARMETVLS 91
                                                                                                                                                                                                                                25; Conservative
                                                                                                                                                                                                                                              14.48;
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                                                                                                                                                                                                                                             Score 88.5; DB Pred. No. 0.23;
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US-10-108-605-305 US-09-987-107-24 US-10-084-994-12

Watson, James D.

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; sequence 22, Application US/10259042
; Publication No. US20030077644A1
                                RESULT 4
US-10-259-042-22
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LENGTH: 299
TYPE: PRT
ORGANISM: Mouse
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LENGTH: 299
TYPE: PRT
ORGANISM: Mouse
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILE REFERENCE: 11000.1011c4U
CURRENT APPLICATION NUMBER: US/09/866,050A
CURRENT FILING DATE: 2001-05-24
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TITLE OF INVENTION: Compositions Isolated From Skin Cells
TITLE OF INVENTION: and Methods for Their Use
                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                      Query Match
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SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Watson, James D.
APPLICANT: Strachan, Lorna
APPLICANT: Sleeman, Matthe
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CURRENT FILING DATE: 2001-05-24
NUMBER OF SEQ ID NOS: 725
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                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQ ID NOS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Murison, James G.
APPLICANT: Kumble, Krishanand D.
TITLE OF INVENTION: Compositions Isolated From Skin Cells
TITLE OF INVENTION: and Methods for Their Use
FILE REFERENCE: 11000.1011c4U
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                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE: FastSEQ for Windows Version 4.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  38 ACHARKGNVSCPLIASLOGSSGTHCEEA-----SSLAEHKLKDVREKMADLARMETVLS 91
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             77 --- CACRNGGLCHATNGSCSCPLGWMGPHCE 104
                                                                                                           77 --- CACRNGGLCHATNGSCSCPLGWMGPHCE 104
                                                                                                                                            92 ELVCA-----CHARKGNVSCPSAWSHPQFE 116
                                                                                                                                                                                41 ACDPVSGTCICP----PGKTGGHCERGCPQDRFGKGCEHK---
                                                                                                                                                                                                                    38 ACHARKGNVSCPLIASLQGSSGTHCEEA-----SSLAEHKLKDVREKMADLARMETVLS 91
                                                                                                                                                                                                                                                                         Local Similarity
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Sleeman, Matthew
Onrust, Rene
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Sleeman, Matthew
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                                                                                                                                                                                                                                                        Score 88.5; DB 9;
Pred. No. 0.23;
2; Mismatches 25;
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; SEQ ID NO 22
; LENGTH: 337
; TYPE: PRT
; ORGANISM: Mus sp.
US-10-259-042-22
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Patent No. US20020048763A1
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Best Local Similarity
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TITLE OF INVENTION: Diagnosis and Treatment of Diseases Caused by Mutations in CD7
FILE REFERENCE: SAG 0105 PUS
CURRENT APPLICATION NUMBER: US/10/259,042
CURRENT FILING DATE: 2002-09-27
RUMBER OF SEC ID NOS: 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: US 60/180,312
PRIOR FILING DATE: 2000-02-04
PRIOR APPLICATION NUMBER: US 60/207,456
PRIOR FILING DATE: 2000-05-26
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TITLE OF INVENTION: HUMAN GENOME-DERIVED SINGLE EXON NUCLEIC ACID PROBES USEFUL FO TITLE OF INVENTION: GENE EXPRESSION ANALYSIS BY MICROARRAY FILE REFERENCE: Acomica-X-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Penn, Sharron G. APPLICANT: Rank, David R. APPLICANT: Hanzel, David K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/864,761
                                                                                                                                                                                                                                                                          PRIOR FILING DATE: 2001-01-30
PRIOR APPLICATION NUMBER: PCT/US01/00665
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: US (
                                                                                                                                                                                                                                                     PRIOR FILING DATE: 2001-01-3
                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION NUMBER: PCT/US01/00666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR FILING DATE: 2000-09-27
                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: PCT/US01/00668
                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION NUMBER: PCT/US01/00669
                                                                                                                                                                                                                                                                                                                                           PRIOR FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                     RIOR
                                                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: PCT/US01/00667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION NUMBER: GB 24263.6
PRIOR FILING DATE: 2000-10-04
                                                                                        PRIOR APPLICATION NUMBER: PCT/US01/00661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    169 AKTKENLKTEEERRRDLDQRLTSTRETLRRFFSDSSDTCCPCGW 212
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          117 QQLREKISQLGQKEVELQK-----ARKELISSQ--DTLQEKQRTHEDAEQQLQACQAER 168
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     16 KDVREKMADLARMETVLSELVCACHARKGNVSCPLIASLQGSSGTH------CEEAS 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               67 SLAEHKLKDVREKMADLARMETVLSELVCACHARKGNVSCPSAW 110
                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: PCT/US01/00664
                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 2001-01-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER:
                   FILING DATE: 2001-01-30
APPLICATION NUMBER: PCT/US01/00670
FILING DATE: 2001-01-30
                                                                                                                                                             FILING DATE: 2001-01-30
                                                                                                                                                                                APPLICATION NUMBER: PCT/US01/00663
APPLICATION NUMBER: US 60/234,687
                                                                                                                  FILING DATE: 200
                                                                                                                                   APPLICATION NUMBER: PCT/US01/00662
                                                                                                                                                                                                     FILING DATE: 2001-01-30
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Chen, Wensheng
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Pred. No. 14;
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Q
                                                                                                                                                                    ; LENGTH: 474
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-084-994-11
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                                                                                  Matches
                                                                                                                            Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                               SEQ ID NO 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 11, Application US/10084994
Publication No. US20030023070A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: EXPRESSED IN
                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION NUMBER: PCT/US00/23663
PRIOR FILING DATE: 2000-08-29
PRIOR APPLICATION NUMBER: US 60/151,348
PRIOR FILING DATE: 1999-08-30
NUMBER OF SEQ ID NOS: 36
                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT APPLICATION NUMBER: US/10/084,994
CURRENT FILING DATE: 2002-03-01
PRIOR APPLICATION NUMBER: US 09/790,621
PRIOR FILING DATE: 2001-02-23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Ni et al.
TITLE OF INVENTION: Attractin-Like Polynucleotides, Polypeptides, and Antibodies
FILE REFERENCE: PT011F1C1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
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                                                                                                                                                                                                                                                                               SOFTWARE: PatentIn Ver. 3.1
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PRIOR FILING DATE: 2001-01-29
NUMBER OF SEQ ID NOS: 49117
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              OTHER INFORMATION: MAP TO AP000215.1
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38 ACHARKGNVSCPLIASLOGSSGTHCEEA---SSLAEHKLKDVREKMADLARMETVLSELV 94
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         111 ----SHPQFEK 117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          139 QKHCEALR-----REK-----EVSATLKSTVEALHTQKRELRCSLEREREKPAWL 183
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 184 QAELEQSHPRLKE 196
                                                                                                  Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    59 GTHCEEASSLAEHKLKDVREKMADLARMETVLSELVCACHARKGNVSC-----PSAW- 110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              91 CVHQDTQAHHALLQKLKEEKSRVVDLQAMLEKVQQQ----ALHSQQ-----QLEAEA 138
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           4 CEEASSLAEH----KLKDVREKMADL-ARMETVLSELVCACHARKGNVSCPLIASLQGSS 58
                                                                             24; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION: EXPRESSED IN FETAL LIVER, SIGNAL = 9.2 INFORMATION: EST_HUMAN HIT: BF375387.1, EVALUE 2.00e-37 INFORMATION: SWISSPROT HIT: 095613, EVALUE 1.00e-107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Similarity
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                                                                                                11.6%;
26.7%;
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23.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              18; Mismatches
                                                                        8; Mismatches
                                                                                                Score 71; DB
Pred. No. 23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         IN HEART, SIGNAL = 6.8
IN HBL100, SIGNAL = 1
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IN BT474, SIGNAL - 7.4
IN BONE MARROW, SIGNAL - 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IN LUNG, SIGNAL = 10
IN HELA, SIGNAL = 13
IN ADULT LIVER, SIGNAL =
IN BRAIN, SIGNAL = 9.9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 71; DB
Pred. No. 11;
                                                                                                                  DB 9; Length 474;
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                                                                      24; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          38; Indels 46;
                                                                   34; Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
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// OTHER INFORMATION: Description of Artificial Sequence: ALP
// OTHER INFORMATION: polypeptide sequence
US-10-020-215-2
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; Publication No. US20030008347A1
; GENERAL INFORMATION:
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  Query Match
Best Local Similarity
                                                                                                                                                                                                                                            SEQ ID NO 2
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                                                                                                                                                                                                                                                                                                                                               APPLICANT: PLOWNAN, GREGORY
APPLICANT: PELES, EIOR
TITLE OF INVENTION: DIAGNOSIS AND TREATMENT OF ALP RELATED DISORDERS
FILE REFERENCE: 038602/1290
CURRENT APPLICATION NUMBER: US/10/020,215
CURRENT FILING DATE: 2001-12-18
PRIOR APPLICATION NUMBER: 09/095,443
PRIOR APPLICATION NUMBER: 09/095,443
PRIOR FILING DATE: 1998-06-10
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Best Local Similarity
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APPLICANT: Willis, Cynthia R.
APPLICANT: Willis, Cynthia R.
TITLE OF INVENTION: Methods for Regulating Vascularization Using GEF
TITLE OF INVENTION: Containing NEK-Like Kinase (GNK)
FILE REFERENCE: Immunex GNK/SGNK PCT
CURRENT APPLICATION NUMBER: US/09/884,001
CURRENT FILING DATE: 2001-06-18
PRIOR APPLICATION NUMBER: 60/113,003
PRIOR FILING DATE: 1998-12-18
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                                                                                                                                                                                                                                                                                      PRIOR APPLICATION NUMBER: 60/049,477
PRIOR FILING DATE: 1997-06-11
NUMBER OF SEQ ID NOS: 10
                                                                                                                                                                                                                                                                SOFTWARE: PatentIn Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Bird, Timothy A. APPLICANT: Peschon, Jacque APPLICANT: Sims, John E.
                                                                                                                                                          ORGANISM: Artificial Sequence
                                                                                                                                                FEATURE:
                                                                                                                                                                                               TYPE: PRT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: PRT
                                                                                                                                                                                                                     LENGTH: 1274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     437 KELSAQMELLRQEVKEKEADFLAQEAQLLEELEASHITEQQLRASLWAQEAKAAQLQLRL 496
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         497 RSTESQLEALAAEQQPGNQAQAQAQLASLYSALQQALGSVCESRPELSGGGDSAPSVW 554
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      58 SGTHCEEASSLAEHKLKDVREKMADLARMETVLSE-LVCACHARK----GNVSCPSAW 110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           32;
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Virca, G. Duke
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  11.6%;
24.6%;
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Score 71;
Pred. No.
DB 9;
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                      Length 1274;
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; ORGANISM: Mus musculus
US-10-037-182-12
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                                                                                                                                                                                                                                                                                                                                                                     Sequence 10, Application US/10037182 Publication No. US20030044899A1 GENERAL INFORMATION:
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APPLICANT: Doi, Masayuki
APPLICANT: Thyboll, Jill
TITLE OF INVENTION: Recombinant Laminin 10
FILE REFERENCE: 99-274-F
                                         SOFTWARE: PatentIn Ver.
SEQ ID NO 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/10/037,182
CURRENT FILING DATE: 2001-12-21
PRIOR APPLICATION NUMBER: 60/257,449
PRIOR FILING DATE: 2000-12-21
PRIOR APPLICATION NUMBER: 60/279,282
PRIOR APPLICATION NUMBER: 60/279,282
PRIOR FILING DATE: 2001-03-28
NUMBER OF SEQ ID NOS: 36
                                                                                                                                                                                                      APPLICANT: Thyboll, Jill
TITLE OF INVENTION: Recombinant Laminin 10
FILE REFERENCE: 99-274-F
CURRENT APPLICATION NUMBER: US/10/037,182
CURRENT FILING DATE: 2001-12-21
                                                                    PRIOR FILING DATE: 2001-03-28
NUMBER OF SEQ ID NOS: 36
SOFTWARE: Patentin Ver. 2.0
                                                                                                                                 PRIOR APPLICATION NUMBER: 60/257,449
PRIOR FILING DATE: 2000-12-21
PRIOR APPLICATION NUMBER: 60/279,282
                                                                                                                                                                                                                                                                                                                            APPLICANT: Tryggvason, Karl
APPLICANT: Doi, Masayuki
TYPE: PRT
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                        ENGTH: 1786
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           116 GQAGAISITS 125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             y Match 11.6%; Score 71; DB 9; Length 1725; Local Similarity 25.6%; Pred. No. 1.1e+02; Local Similarity 18; Mismatches 17; Indels 26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   65 ALSVRPDTVRNLVQSMQVLSGVFTD-----VEASLKDIRDLLEEDELLEQKFQEAV---- 115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               39 CHARKGNVSCPLIASLQGSSGTHCEEASSLAEHKLKDVREKMADLARMETVLSELVCACH 98
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99 ARKGNVSCPS 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        71 HKLKDVREKMADLARMETVLSE 92
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; ORGANISM: Mus musculus US-10-037-182-10
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Matches 21; Conserve
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 7
LENGTH: 1786
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                                                                                                                                                                                                                                                                                                                                                                                             Sequence 260, Application US/10082830 Publication No. US20030077604A1 GENERAL INFORMATION:
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SEQ ID NO 260
LENGTH: 2383
                                                                                                                                                                                                                                                                                             APPLICANT: Sun, I
APPLICANT: Recip
APPLICANT: Salce
APPLICANT: Liu,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: PRT
ORGANISM: MUS MUSCULUS
PUBLICATION INFORMATION:
DATABASE ACCESSION NUMBER: Swissprot P02469
DATABASE ENTRY DATE: 1989-07-01
                                                           CURRENT APPLICATION NUMBER: US/10/082,830
CURRENT FILING DATE: 2001-10-29
PRIOR APPLICATION NUMBER: 60/243,802
PRIOR FILING DATE: 2000-10-27
NUMBER OF SEQ ID NOS: 282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/938,275
CURRENT FILING DATE: 2001-08-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TITLE OF INVENTION: Therapeutic and Diagnostic Applications TITLE OF INVENTION: of Laminin and Laminin-Derived Protein Fragments FILE REFERENCE: PROTEO.P03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Gerardo Castillo APPLICANT: Alan Snow.
                                                                                                                                                                                             APPLICANT: Turner, Leah TITLE OF INVENTION: Compositions and Methods Relating to Breast Specific TITLE OF INVENTION: Genes and Proteins FILE REFERENCE: DEX-0249
                                                 SOFTWARE: PatentIn Ver.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1546 ----DIRERVETLSQVEVILQQ 1563
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    71 HKLKDVREKMADLARMETVLSE 92
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Salceda, Susana
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4

; ORGANISM: Mus musculus US-09-796-753-116

SEQ ID NO 116

TYPE: PRT LENGTH: 497 NUMBER OF SEQ ID NOS:

PRIOR FILING DATE: 2000-09-20
PRIOR APPLICATION NUMBER: 09/6
PRIOR FILING DATE: 2000-09-30

09/677,751 09/665,666 09/606,317

PRIOR APPLICATION NUMBER: 09/ PRIOR FILING DATE: 2000-06-29 PRIOR APPLICATION NUMBER: 09/

Matches Query Match

22;

Conservative

6; Mismatches Score 70.5; DB 9; Pred. No. 28;

28;

Gaps

4,

Length 497; Indels 25;

Local Similarity

11.5%; 27.2%;

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Publication No. US20030027998A1
                                                                                                                                                                 PRIOR
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CURRENT FILING DATE: 2001-03-01
PRIOR APPLICATION NUMBER: 09/183,175
PRIOR FILING DATE: 1998-10-30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: McCarthy, Sean A.
TITLE OF INVENTION: SECRETED PROTEINS AND USES THEREOF
FILE REFERENCE: 7853-227-999
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                                                                                                                                                                                                                                   A APPLIANCE 1999-12 JR FILING DATE: 1999-12 OF APPLICATION NUMBER: 09/474 OR APPLICATION NUMBER: 1999-12-29 IOR APPLICATION NUMBER: 09/47 IOR APPLICATION NUMBER: 09/475 OR 1999-12-29
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R APPLICATION NUMBER: 09/57

DR APPLICATION NUMBER: 09/57

DR APPLICATION NUMBER: 09/57

DR APPLICATION NUMBER: 09/57
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                            FILING DATE: 2000-06-22
APPLICATION NUMBER: 09/
FILING DATE: 2000-07-31
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(APPLICATION NUMBER: 09/3
APPLICATION TO NAME: 1999-06-29
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APPLICATION NUMBER: 09/
FILING DATE: 1998-12-30
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APPLICATION NUMBER: 09/2
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FILING DATE: 1999-06-30
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APPLICATION NUMBER: UY/.
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APPLICATION NUMBER: UY/.
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2000-06-29
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               09/606,565
                                               09/630,334
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US-10-045-792-8

Sequence 8, Application US/10045792 Publication No. US20030003563A1

GENERAL INFORMATION:

APPLICANT:

Moarefi, Ismail Darnell, Jr., James E. Vinkemeier, Uwe

Kuriyan,

John

INFORMATION FOR SEQ ID NO: 8:

TELEX: 133521

SEQUENCE CHARACTERISTICS:

TYPE: amino acids STRANDEDNESS: single

NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-194
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201-487-5800
TELEFAX: 201-343-1684

ATTORNEY/AGENT INFORMATION:

APPLICATION NUMBER: US/09/012,710 FILING DATE: <Unknown>

PRIOR APPLICATION DATA:

CURRENT APPLICATION DATA:

SOFTWARE: PatentIn Release #1.0, Version #1.30

APPLICATION NUMBER: US/10/045,792 FILING DATE: 19-Oct-2001 CLASSIFICATION: <Unknown>

ZIP: 07601 COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk

COUNTRY:

USA

CITY: Hackensack STATE: New Jersey

STREET: 411 Hackensack Avenue, 4th Floor

COMPUTER: IBM PC OPERATING SYSTEM:

IBM PC compatible SYSTEM: PC-DOS/MS-DOS

CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson

NUMBER OF SEQUENCES:

TITLE OF INVENTION: A CRYSTAL OF THE N-TERMINAL DOMAIN OF A STAT PROTEIN AND METHODS OF USE THEREOF

TOPOLOGY: linear MOLECULE TYPE: protein HYPOTHETICAL: NO

RESULT 14

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131 HGGTCHPQDGSCICTPGWTGP 151 96 --- ACHARKGNVSCPSAWSHP 113

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RESULT 15
US-10-038-010-56
US-10-038-010-56
Sequence 56, Application US/10038010
Publication No. US20030040089A1
GENERAL INFORMATION:
APPLICANT: HYBRIGENICS
APPLICANT: HYBRIGENICS
ITITLE OF INVENTION: Protein-protein interactions in adipocyte cells
FILE REFERENCE: B4767A
CURRENT APPLICATION NUMBER: US/10/038,010
CURRENT FILING DATE: 2002-07-23
PRIOR APPLICATION NUMBER: US 60/259,377
PRIOR APPLICATION NUMBER: US 60/259,377
PRIOR FILING DATE: 2001-01-02
NUMBER OF SEQ ID NOS: 67
SOFTWARE: Patentin version 3.1
SEQ ID NO 56
SEQ ID NO 56
SEQ ID NO 56
SEQ TO TYPE: PRT
ORGANISM: Homo sapiens
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NAME/KEY: STAT3: Transcription factor
LOCATION: (1)..(770)
OTHER INFORMATION:
US-10-038-010-56
Search completed: May 28, 2003, 10:38:14 Job time: 59 secs
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                                                                                                                                                                                                                                                                                                                  Query Match 11.5%; Score 70.5; DB 9; Length 770; Best Local Similarity 23.3%; Pred. No. 47; Matches 24; Conservative 20; Mismatches 38; Indels 21; Gaps
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                                                                                                    126 GGQANHPTAAVVTEKQQMLEQHLQDVRKRVQDLEQKMKVVENL 168
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                                                                                                                                                           56 GSSGTH-----CEEASSLAEHKLKDVREKMADLARMETVLSEL 93
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 2000000000
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

REFERENCE AUTHORS TITLE JOURNAL	SOURCE	VERSION VERSION	AX473152 LOCUS DEFINITION	, 1-1			43	41		ω.	ა ა 7		ω	c 31	30.	> 2 9 8		25 5	24	222		19	18	16					ω,		4 10		1 2	Result No.	
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lat,J.J. , recombinant host c 18-APR-2002; RESEARCH FOUNDATION,		71	321 bp t W00230962.		ALIGNMENTS	ARMERGE7	ECMERTREL	AF461013	ASP250860 ASP245842	PSPY18976	ECTREMER1	ACMERGE2 ECMERGE6	PPU344068	PSU90263	RGE	FMER	PLMMEROSA	ASTIMER	PLMMERGEL	AF092070	AF348706	PSU80214	PSMERGE9	PFMERGE10	EAMERGE8	STYPPHCM1	AP000342	AF071413	R1004	PFL422225	150 222	7316	731 731	ID	
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EYWORDS	AX473152.1 GI:22207871		
OURCE	synthetic construct.		
ORGANISM	synthetic construct		
EFERENCE	artificial sequences. 1		
AUTHORS	Summers, A.O. and Caguiat, J.J.		
TITLE JOURNAL	Metal binding proteins, recombinant host cells and metal binding proteins, recombinant host cells and metals wo 0330962-A 3 18-APR-2002; UNIVERSITY OF GEORGIA RESEARCH FOUNDATION, INC. (US)	cells and meth	nods

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61 AAGATGGCCGACTTGGCGCGCATGGAAACCGTGCTGTCTGAACTCGTGTGCGCCTGCCAT 120
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                              61 AAGATGGCCGACTTGGCGCGCATGGAAACCGTGCTGTCTGAACTCGTGTGCGCCTGCCAT 120
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Metal binding proteins, recombinant host cells and methods
Patent: WO 0330962-A 17 18-APR-2002;
UNIVERSITY OF GEORGIA RESEARCH FOUNDATION, INC. (US)
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/db_xref="taxon:32630"
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Submitted (18-DEC-2001) Kholodii G.Y., Russian Academy of Sciences, Sci
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Kholodii,G.Y., Gorlenko,Z.M., Mindlin,S.Z. and Nikiforov,V.G. Distribution of distinct microvariants of Tn5041 in environmental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pseudomonas fluorescens (strain KHP22) transposon Tn5041G, partial sequence (region of insertion of Tn21 homologue).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pseudomonas fluorescens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kholodii,G.Y
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PFL422224
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Seudomonas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Summers, A.O. and Caguiat, J.J.
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                                                                                                                                                                                                                                                                                                                                                      sequence Y09209
                                                  /country="Kyrgyzstan:Khaidarkan"
/note="isolated from mercury mine, ore"
                                                                                                                      /sex="Tra+ (narrow range)"
/plasmid="pKHP22"
                                                                                                                                                                                                                         /strain="KHP22"
transposon="Tn5041G"
                                                                                                                                                                                       /db_xref="taxon:294"
                                                                                                                                                                                                                                                       organism="Pseudomonas fluorescens"
                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
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/db_xref="taxon:623"
/note="Taxon:21 of Plasmid R100"
113 c 146 g 81 t
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Pred. No. 3.3
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          4 ACACACTGCGAGGAGGCCAGCAGCCTGGCCGAACACAAGCTCAAGGACGTGCGCGAGAAG 63
                                                                                                                                                                    RUSSIA
                                                                                                                                                                                               Submitted (18-DEC-2001) Kholodii G.Y.,
                                                                                                                                                                                                                                                                                                Kholodii,G.Y., Gorlenko,Z.M., Mindlin,S.z. and Nikiforov,V.G. Distribution of distinct microvariants of Th5041 in environmental
                                                                                                                                                                             Institute of Molecular Genetics, Kurchatov Sq.
                                                                                                                                                                                                                   Direct Submission
                                                                                                                                                                                                                                      Kholodii,G.Y
                                                                                                                                                                                                                                                                                                                                                                                        Pseudomonas fluorescens.
Pseudomonas fluorescens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PFL42225 445 bp DNA linear Pseudomonas fluorescens (strain KHP25) transposon
                                                                                                                                                                                                                                                                     Unpublished
                                                                                                                                                                                                                                                                                         bacteria
                                                                                                                                                                                                                                                                                                                                                           Pseudomonas
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        sequence (region containing a Tn21 homologue).
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/transl_table=11
/product="MerR protein"
_____149 c 119 g 8
                                          /sex="Tra+ (narrow range)"
/plasmid="pKLH22"
            /country="Kyrgyzstan:Khaidarkan"
/note="isolated from mercury mine, ore"
                                                                                                  /strain="KHP25"
                                                                              /db_xref="taxon:294"
                                                                                                               /organism="Pseudomonas fluorescens"
                                                                                                                                                 Location/Qualifiers
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/rpt_type=INVERTED
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/transposon="Tn21deltaIn2"
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Pred. No. 3.3e-26;
0; Mismatches 6;
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                                                                                                                                                                                            Russian Academy of Sciences,
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                                                                                                                                                                             2, Moscow 123182,
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                                                                                                                                                                                                                                                                                           1 (bases 1 to 3763)
Barrineau, P., Gilbert, P., Jackson, W.J., Jones, C.S., Summers, A.O. and Wisdom, S.
praft entry and sequence in computer readable form for [2] kindly provided by A.O.Summers, 15-SEP-1986. Potential Shine-Dalgarno sequences are located at positions 157-162 (13.1 kd), 590-596 (12.4 kd), 1740-1745 (59 kd) and 545-542 (15.9 kd). A single 38 bp inverted repeat, which delimits the leftward end of Tn21, Tn4 and Tn501 extends from nucleotide 65-102. A promoter region for the
                                                                                                                                                                                                                                                                                                                                                                                       merA gene; merR gene; merT gene; mercuric reductase.
Plasmid NR1 (IncFII) from E.coli DNA, clone pDB7.
                                                                                                                    Unpublished (1986)
[2] reviser (1986)
                                                                                                                                                          2 (bases 1 to 3763)
Summers, A.O.
                                                                                                                                                                                                                                                                                                                                                                                                                                               Plasmid NR1 mercury resistance K03089
                                                                                                                                                                                                                                                    plasmid NR1
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                                                                                                                                                                                                                                                                           The DNA sequence of the mercury resistance operon of the IncFII
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/protein_id="0AD19592.1"
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/db_xref="G1:19848213".1"
/db_xref="G1:19848213".1"
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/translation="verlineryQrkGlLPepDkPyGSIRRYGEADVVRVKFVKSAQRLG
FSLDEIAELLRLDDGTHCEEASSLAEHKLKDVREKMADLARMETVLSELVCACHARKG
RVSCPLIASLQGEAGLARSAMP"
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/transposon="Tn21deltaIn2"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement(98. .532)
/note="15.9 kd merR protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="GI:455296"
/translation="mennlentfigyfakaagynyefireygrkgilrepdkpygsir
/translation="mennlentfigyfakaagynyefireygrkgilrepdkpygsir
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="GI:150392"
/translation="mraksaifsrtslslcsarllassqwvpsssrnssaissrlnps
rcadetnftrttsasp"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /translation="magahefrohgfharqvghllahvlelvfgoaagllavgaivep
QQLGNLvQTEPOPLCRFHEFHPNHVRLPIAADAAVRLVRFPQQALALIEADCLHVDPG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /plasmid="Plasmid NR1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /protein_id="AAB59073.1"
/db_xref="GI:150391"
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                                                                                                                                           /translation="MGLMTRIADKTGALGSVVSAMGCAACFPALASFGAAIGLGFLSQ
YEGLFISRLLPLFAALAFLANALGWFSHRQWLRSLLGMIGPAIVFAATVWLLGNWWTA
NLMYVGLALMIGVSIWDFVSPAHRRCGPDGCELPAKRL"
                                                                                                                                                                                                                                                                                                                                                                                                         /translation="mkklfaslalaaavapvwaatgtvtlavpgmtcaacpitvkkal
skvegvtkvdvgfekreavvtfddtkasvqkltkatadagvpssvkq"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="G1:150393"
/translation="MSEPQNGRGALFAGGLAAILASTCCLGPLVLVALGFSGAWIGNL
TVLEPYRPLFIGAALVALFFAWKRIYRPVQACKPGEVCAIPQVRATYKLIFWIVAVLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /transl_table=11
/protein_id="AAB59075.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /transl_table=11
/protein_id="AAB59074.1"
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/protein_id="AAB59076.1"
/db_xref="GI:150394"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               note="6.5 kd protein"
                                                                                                                                                                                                                                   /transl_table=11
/protein_id="AAB59077.1"
/db_xref="GI:150395"
                                                                                                                                                                                                                                                                                                                                                1279. .1701
/note="15.0 kd merTC protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="9.4 kd merTB protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          JVALGEPYVVPFFY"
/protein_id="AAB59078.1"
                                                                                       /note="Hg(II) reductase (59.0 kd merA)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                codon_start=
                           transl_table=11
                                                                                                                                                                                                                                                                                                                           'codon_start=1
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RESULT 8
R1004/c
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MEDLINE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      175 CGAAAGGGGAATGTTTCCTGCCCGTTGATCGCGTCACTACAGGGCGAAGCAGGC 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           124 CGAAAGGGGAATGTTTCCTGCCCGTTGATCGCGTCACTACAGGGATCCTCAGGC 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 (bases 849 to 2189)
Misra,T.K., Brown,N.L., Fritzinger,D.C., Pridmore,R.D.,
Barnes,W.M., Haberstroh,L. and Silver,S.
Mercuric ion-resistance operons of plasmid R100 and transposon
Tn501: the beginning of the operon including the regulatory rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                168;
                                                                                                                                Ohtsubo, H., Nyman, K., Doroszkiewicz, W. and Ohtsubo, E. Multiple copies of iso-insertion sequences of IS1 in Shigella dysenteriae chromosome
                                                                                                                                                                                                                                 Ohtsubo, H. and Ohtsubo, E. Nucleotide sequence of an insertion element, I Proc. Natl. Acad. Sci. U.S.A. 75 (2), 615-619
                                                                                                                                                                                                                                                                                                                                                                       4 of
                                                                                                                                                                                                                                                                                                                                                                                                                                                           R1004 S747 bp DNA linear BCT 01-00 Plasmid R100 putative (insh), putative (insh), merR (merR), putative (merT), merC (merC), mercuric reductase (merA), and
                                                                                            6265806
                                                                                                                      Nature 292 (5824), 640-643 (1981)
                                                                                                                                                                                                                                                                                                                                                    Escherichia coli.
                                                                                                                                                                                                                                                                                                                                                                                        J01730.1 GI:151742
IS1 insertion sequence; merC gene; merR gene; merT gene; mercuric
                                                                                                                                                                                                                                                                                                        Escherichia.
                                                                                                                                                                                                                                                                                                              Bacteria; Proteobacteria; gamma subdivision;
                                                                                                                                                                                                                                                                                                                                      Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                     reductase; transposon.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  putative (merD) genes,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /citation=[1]
/replace="" |
696 a 1198 c 1189 g
117 bp upstream of EcoRII site.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           similarity 96.6%;
                                                                                                                                                                                          (sites)
                                                                                                                                                                                                                                                                                        (bases 1 to 5747)
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/replace=""
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1890
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATVGYSEAEAHHDGIKTDSRTLTLDNVPRALANFDTRGFIKLVVEEGSGRLIGVQAVA
PEAGELIQTAALAIRNRMTVQELADQLFPYLTMVEGLKLAAQTFNKDVKQLSCCAG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /citation=[1]
/replace=""
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /translation="MSTLKITGMTCDSCAVHVKDALEKVPGVQSADVSYAKGSAKLAI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /db_xref="GI:150396"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 164.4; DB 1; Length 3763; Pred. No. 2.9e-26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  complete
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                                                                                                                                                                                                                                                    IS1
                                                                                                                                                                                                                                                                                                              Enterobacteriaceae;
   regulatory region
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Three R100 derived small circular plasmids (pSM1, pSM2, pSM5) contain ISIR. pSM2 consists of map units 82.7-89.3 (the 3' end of ISIR) in circularized form. pSM1 is the same as pSM2, except for a deletion of map units 87.4-88.6. pSM 15 consists of map units 83.4-89.3 in circularized form.

Potential -35 regions are found at positions 980-984 and 1402-1406 and -10 regions at positions 999-1006 and 1425-1431. Unidentified reading frames are found at positions 2143-2565, 4688-4924 (gtg start codon), and 4921 to 5593. [4] noted two other ORF's in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence for (3), [5] and [4] kindly provided on tape by T.K.Misra ISI from [1] was renamed ISIR after [2] discovered that there are several ISI iso-insertion sequences. The 5 and 3' ends of ISIR are approximate inverted repeats. [2] found the CDS regions annotated below conserved among several ISIs. Deletion mutations in either of these two coding frames or in the two ends of ISIR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        start codon), and 4921 to 5593. vicinity of the merR gene.
[2] sites; insA and insB spans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               5 (bases 4348 to 5747)
Brown, N.L., Misra, T.K., Winnie, J.N., Schmidt, A., Lien, C., Sieff, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and Silver, S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mercuric reductase structural genes from plasmid R100 and transposon Tn501: functional domains of the enzyme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Misra, T.K., Brown, N.L., Haberstroh, L., Schmidt, A., Goddette, D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         and the first two structural genes Proc. Natl. Acad. Sci. U.S.A. 81 (
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                                                                /transl_table=11
/protein_id="AAA92259.1"
/protein_id="AAA92259.1"
/db_xref="GI:151748"
/translation="MDEQWGYVGAKSRQRWLFYAYDRLRKTVVAHVFGERTMATLGRL/
MSLLSPEDVVIWMTDGWPLYESRLKGKLHVISKRYTQRIERHHUNLRQHLARLGRKSL
                                SFSKSVELHDKVIGHYLNIKHYQ" 929. .966
                                                                                                                                                                                                                                                                                                                                                                             /protein_id="AAA92258.1"
/db_xref="GI:294459"
/translation="MASVSISCPSCSATDGVVRNGKSTAGHQRYLCSHCRKTWQLQFT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /gene="
158..4
/note="Tn21 inverted repeat"
                                                                                                                                                                                                             /codon_start=1
                                                                                                                                                                                                                                   /note="putative"
                                                                                                                                                                                                                                                           /gene-"
                                                                                                                                                                                                                                                                                                                                                             YTASQPGTHQKIIDMAMNGVGCRATARIMGVGLNTIFRHLKNSGRSR"
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/db_xref="taxon:562"
/insertion_seq="IS1"
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/clone="pSM[1,2,15],
/plasmid="R100"
103. .870
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ACACACTGCGAGGAGGCCAGCAGCCTGGCCGAACACAAGCTCAAGGACGTGCGCGAGAAG 63
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                                           Conservative
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SKYEGVSKYDVGFEKREAVVTFDDTKASVQKLTKATADAGYPSSVKQ"
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TVLEPYRPLFIGAALVALFFAWKRIYRPVQACKPGEVCAIPQVRATYKLIFWIVAVLV
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/db_xref="GI:151749"
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/Translation-*MSTLKITGMTCDSCAVHVKDALEKVPGVQSADVSVAKGSAKLAI
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IQLKNDGGERVVAFDRCLLATGASPAVPPIPGKLKDTPYMTSTEALVSETIPKRLAVIG
SSVYALELAQAFARKGAKYTILARGASPAVPPIPGKAVVAAFRKGGIEVREHTQASQ
VAYINGEGDDGEFVLTTAHGELRADKLLVATGRAPNTRKLALDATGVTLTPQGAIVIDP
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ATVGYSEAEAHHDGIKTDSRTLTLDNVPRALANFDTRGFIKLVVEEGSGRLIGVQAVA
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/product="mercuric_reductase"
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                                                                                                                                                                                                                        /protein_id="AAA92264.1"
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/db_xref="GI:151752"
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|gene="merD"
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                                                                                                                                                                                                                                                                                                                      Silver,S. Mercuric reductase structural genes from plasmid R100 and transposon Tn501: functional domains of the enzyme Gene 34 (2-3), 253-262 (1985) 85232071
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          and Wisdom, S.

The DNA sequence of the mercury resistance operon of the IncFII plasmid NR1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 (bases 18411 to 19672)
Risra,T.K., Brown,N.L., Fritzinger,D.C., Pridmore,R.D.,
Maisra,T.K., Brown,N.L., and Silver,S.
Barnes,W.M., Haberstroh,L. and Silver,S.
Mercuric ion-resistance operons of plasmid R100 and transposon
Tn501: the beginning of the operon including the regulatory region
and the first two structural genes
and the first two structural genes
Proc. Natl. Acad. Sci. U.S.A. 81 (19), 5975-5979 (1984)
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Barrineau, P., Gilbert, P., Jackson, W.J., Jones, C.S., Summers, A.O.
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                                                                     6 (bases 3057 to 4105)
Hyde, D.R. and Tu,C.P.
tnpM: a novel regulatory gene that enhances Tn21 transposition and suppresses cointegrate resolution
CCOL 42 (2), 629-638 (1985)
                                                                                                                                                                                                                         Rogowsky,P., Halford,S.E. and Schmitt,R.

Definition of three resolvase binding sites at the res loci of Tn21
and Tn1721
                                                                                                                                                                                                                                                                                                                                                                                                               4 (bases 16253 to 18549)
Misra,T.K., Brown,N.L., Haberstroh,L., Schmidt,A., Goddette,D.
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7 (bases 14935 to 15434)
Brown, N.L., Misra, T.K., Winnie, J.N., Schmidt, A.,
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                                                                   Levesque,C., Brassard,S., Lapointe,J. and Roy,P.H. Diversity and relative strength of tandem promoters for the antibiotic-resistance genes of several integrons
                                                           Gene 142 (1), 49-54 (1994)
                                                                                                                                                                                                                                                                                                                                                   14 (bases 14967 to 15674)
Allmeier,H., Cresnar,B., Greck,M. and Schmitt,R.
Complete nucleotide sequence of Tn1721: gene organization and novel gene product with features of a chemotaxis protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mercier, J., Lachapelle, J., Couture, F., Lafond, M., Vezina, G., Boissinot, M. and Levesque, R. C. Structural and functional characterization of tnpI, a recombinase locus in Tn21 and related beta-lactamase transposons
J. Bacteriol. 172 (7), 3745-3757 (1990)
                       8181756
                                                                                                                                                                                                                          regulator
                                                                                                                                                                                                                                Untwist and shout: a heavy metal-responsive transcriptional
                                                                                                                                                                                                                                                              Summers, A.O.
                                                                                                                                                                                                                                                                                                                                            Gene 111 (
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Guerineau,F., Brooks,L. and Mullineaux,P.
Expression of the sulfonamide resistance gene from plasmid
Plasmid 23 (1), 35-41 (1990)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Stokes,H.W. and Hall,R.M.
A novel family of potentially mobile DNA elements encoding site-specific gene-integration functions: integrons Mol. Microbiol. 3 (12), 1669-1683 (1989)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    13 (bases 4106 to 5438)
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Ward, E. and Grinsted, J.
The nucleotide sequence of the tnpA gene of Tn21
Nucleic Acids Res. 15 (4), 1799-1806 (1987)
87146495
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86174347
(bases 4492 to 8992)
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Submitted (27-NOV-1989)
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24 (bases 1 to 19672)
Liebert, C.A., Hall, R.M. and Summers, A.O.
Transposon Tn21, flagship of the floating genome
                                                    Direct Submission
                                                                                  GenBank Accession Number x12870 27 (bases 7540 to 14934)
                                                                                                                                                      Sundstroem, L
                                                                                                                                                                 correction of sequence errors 26 (bases 4106 to 7539)
                                                                                                                                                                                                      Unpublished
                                                                                                                                                                                                                                   Partridge, S.R. and Hall, R.M. In34, a complex In5-like cla
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Collis,C.M., Kim,M.J., Stokes,H.W. and Hall, N.M. Binding of the purified integron DNA integrase Intl1 to integronand cassette-associated recombination sites Mol. Microbiol. 29 (2), 477-490 (1998)
                                                                                                                                                                                                                                                                   25 (bases 7540 to 14934)
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                                                                                                                                                                                                                                                                                                                                                                                                                                      attI1 site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gene cassettes: a new class of mobile element Microbiology 141 (Pt 12), 3015-3027 (1995)
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Recchia,G.D. and Hall,R.M.
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(bases 5343 to 6256)

Na Kim,M.J., Stokes,H.W. and Hall,R.M.
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Hrown,H.J., Brookes,D.E. and Stokes,H.W.
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(bases 4048 to 4159; 14945 to 15031)
Antrom D Skold.O., Swedberg,G., Flensburg,J., Roy,P.H.
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Bacteriol. 176 (11), 3257-3268 (1994)
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 51.2%;
96.6%;
Score 164.4; DB 1
Pred. No. 2.7e-26;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Direct Submission
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Chen, J.-H. and Chen, J.-Y.
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TnSF1, a Tn21-like transposon in Shigella flexneri
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                                                                                                                                                                                                                                                                             /product-"putative transposase"
/protein_id="AAG14402.1"
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NEFRASKAKSTGHINPKYGSSPGRTFYTHISDQYAPFHTKVVNNGLRDSTYVLDGLLY
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APEFLAVLKLRAAPAAKNYLDA IEVLRGMNTUNARKLPADAPTGF IKPRWQKLVMTDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement(34. .3000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement(14272.
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                                                                                                                                                                                                                                                                                                                                                     DWSEARVDDPAIDMAAHLMVFGKEGLAKLLLTYETAGGRVWPRLAHHIAERLAFGAVT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        function="may confer resistance to erythromycin"
                                                                                                                                                         function="confers resistance to kanamycin"
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                                                 TITLE
                                                                                                                                                                                                                   TITLE
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                                                                                                                                                                                                                                                                                                                         yahA; istA; istB; ybbA; sull; gacEdeltal; aadAl; intR; tniBdeltal; tnpA; ybjA; cat; insA; sull; gacEdeltal; aadAl; intR; tnpM; tnpR; tnpA; ybjA; cat; insA; insB; ycdA; ycdB; stbB; stbA; ycgA; ycgB; ychA; yciB; ycjA; ycjB; ydaA; ydbA; ydcA; yddA; ycgB; ydaA; ydbA; ydcA; yddA; ysdB; ydaA; ydbA; ydcA; yddA; ssb; ydeA; ydeB; ydgA; ydfB; yefA; xtraY; traY; traB; traE; traE; traB; 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26482 ATGGCCGACTTGGCGCGCATGGAAACCGTGCTGTCTGAACTCGTGTGGGGCCTGCCATGCA 26541
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26422 ACCCACTGCGAGGAGGCCAGCAGCCTGGCCGAACACAAGCTCAAGGACGTGCGCGAGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              64 ATGGCCGACTTGGCGCGCATGGAAAACCGTGCTGTCTGAACTCGTGTGCGCCTGCCCATGCA 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 168;
                                                                      2 (bases 1 to 94281)
Sampei, G. and Mizobuchi, K.
                                                                                                                                                    Sampei, G. and Mizobuchi, K. Organization and diversification of plasmid genomes: complete nucleotide sequence of the R100 genome
                                          Direct Submission
                                                                                                                                             Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 4 ACACACTGCGAGGAGGCCAGCAGCCTGGCCGAACACAAGCTCAAGGACGTGCGCGAGAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Plasmid R100 DNA, complete sequence.
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7506 c 7633 g
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         function="confers resistance to ampicillin"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="bla"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    94281 bp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5866 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   6,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BCT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0,
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                                                                                        CDS
                                                                                                                                                       gene
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     repeat_unit
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note="100% identical to gp:R1004_6[MerA of plasmid R100]"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 . 9428
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JOURNAL
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/translation="mSQQANDNSESRFMGLMTRIADKTGALGSVVSAMGCAACFPALA
SFGAAIGLGFLSQYEGLFISRLLPLFAALAFLANALGWFSHRQWLRSLLGMIGPAIVF
AATVWLLGNWWTANLMYVGLALMIGVSIWDFVSPAHRRCGPDGCELPAKRL"
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/protein_id="BAA78788.1"
/db_xref="GI:5103152"
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/transl_table=11
                                                                                                                                                                                                 /note="100% identical to gp:NRIMER_6[MerC of plasmid NR1]"
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                                                                                                                                                                                                                                       /gene="merC"
                                                                                                                                                                                                                                                               /gene="merC"
1234. .1695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="100% identical to gp:NRIMER_5[MerP of plasmid NRI]"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /codon_start=1
/transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement(92. .526)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /specific_host="Shigella flexneri 2b strain
/db_xref="taxon:28399"
/lab_host="Escherichia coli strain K-12"
/note="Plasmid R100 is also referred to as N
join(59. .7369,11456. .19730)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LVALGFPYVVPFFY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="regulatory protein of mer operon"
/protein_id="BAA78785.1"
/db_xref="GI:5103149"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        complement(92.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               'gene="merp"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gene="merp"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            transl_table=11/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  codon_start=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "ARMETYLSELVCACHARKGNVSCPLIASLQGEAGLARSAMP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /codon_start=1
/transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="100% identical to gp:NR1MER_1[MerR of plasmid NR1]"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="merR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="merR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    'note="100% identical to gp:NR1MER_4[MerT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gene="merT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="terminal IR of Tn21"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /plasmid=""
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     gene-"merT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      transposon="Tn21"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   organism="Plasmid R100"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 to as NR1 or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       of.
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CDS

gene

CDS

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repeat_unit
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FDGGIAATTPTIQRTALLAQQQARVDELRHAKYEGILEGNPAITVLHGSARRKDNRNL
IVQLNDGGERVVARDRCLLATGASPAVPPIPGLKDTPYMTSTEALVSETIPKKLAVIG
SSVVALELAQAFARLGAKVTILARSTLFFREDPAIGEAVTAAFRMEGIEVREHTQASQ
VAXINGEGGEFVLTTAHGELRAKKLLVATGRAPNTRKLALDATGVTLTPQGAIVIDP
GMRTSVEHIYAAGDCTDQPQFVYVAAAAGTRAAINMTGGDAALNLTAMPÄVVFTDPQV
ATVGYSEAEAHHDGIKTDSRTLTLDNVPRALANFDTRGFIKLVVEEGSGRLIGVQAVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /translation="mstlkitgmtcdscavhvkdalekvpgvqsadvsyakgsaklai
EVGTSPDALTAAVAGLGYRATLADAPSVSTPGGLLDKKRDLLGRNDKTGSSGALHIAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product="mercuric (ion) reductase"
/protein_id="BAA78789.1"
/db_xref="GI:5103153"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /protein_id="BAA78790.1"
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/translation="MSAYTYSQLAHNAGVSVHIVRDYLVRGLLRPVACTTGGYGVFDD
/translation="MSAYTYSQLAHNAGVSVHIVRDYLVRGLLRPVACTTGGYGVFDD
AALQRLCFVRAAFEAGIGLDALARLCRALDAADGAQAAAQLAVLRQLVERRAALAHL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3459.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     3459. .3821
/gene="merD"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DAQLASMPAERAHEEALP"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   function unknown] "
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          note-"99% identical to gp:R1004_7[MerD of plasmid R100,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           codon_start-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GAFLGEHWGVAALALTGLFVLAVTRLLRAFRGGS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                          4692
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /translation="mtssqpagwtaaelaqaaargqldlhyqplvdlrdhriagaeal
mrwrhprlgllppgqflplaesfglmpeigawvlgeacromhkwqgpawqpfrlainv
sasqvgptfddevkrvladmalpaelleieltesvafgnpalfasfdalraigvrfaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                4051.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /protein_id="BAA78791.1"
/db_xref="GI:5103155"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              transl_table=11/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="100% identical to gp:ECOMERTET_3[urfl, ORF, gene product of plasmid R100]"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="yadA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DDFGTGYSCLQHLKCCPITTLKIDQSFVARLPDDARDQTIVRAVIQLAHGLGMDVIFR
RRLHQLIGRNGCCAASS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /protein_id="BAA78792.1"
/db_xref="GI:5103156"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /codon_start=1
/transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="99% identical to
yene product of plasmid
                                                                                                                                                                                                                                                                                                     4833. .6512
/gene="tniA"
                                                                                                                                                                                                                                                                                                                                                                                                                                              join(4692. .7369,11456. .15691)
/transposon="In2"
QKRFLTKQKRSLAAFHREVTQVCKAQKLRVPARNTVALRIASLDPRKVIRRREGQDAA
                          /translation="MATDTPRIPEQGVATLPDEAWERARRRAEIISPLAQSETVGHEA
ADMAAQALGLSRRQVYVLIRRARQGSGLVTDLVPGQSGGKGKGRLPEPVERVIHELL
                                                                            /product="transposase of In21"
/protein_id="BAA78793.1"
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                                                                                                                                                              transl_table=11
                                                                                                                                                                                        codon_start=1
                                                                                                                                                                                                                   note-"100% identical to gp:TTU42226_8 [TniA of Tn21]"
                                                                                                                                                                                                                                                                                                                                                               'note="terminal IR of In2"
                                                                                                                                                                                                                                                                                                                                                                                          /gene="yaeA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   yaeA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      yadA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               gp:ECOMERTET_4[urf2, putative ORF,
R100]"
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gene

CDS

CDS gene

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REFERENCE
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                                  REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                       KEYWORDS
                                                                                                                                                                                                                                                                                                                                                                                                             VERSION
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pocus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
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                                                                                                                                                                                                                                                                                                                                                    ORGANISM
                                                                         JOURNAL
                                                                                                                                                                                                                                                                        AUTHORS
                                                                                                                TITLE
TITLE
                  AUTHORS
                                                         PUBMED
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     169
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        124 CGAAAGGGGAATGTTTCCTGCCCGTTGATCGCGTCACTACAGGGATCCTCAGGC 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 168;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        64 ATGGCCGACTTGGCGCATGGAAAACCGTGCTGTCTGAACTCGTGTGCGCCTGCCATGCA 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              4 ACACACTGCGAGGAGGCCAGCAGCCTGGCCGAACACAAGCTCAAGGACGTGCGCGAGAAG
                                                                                        Parkhill, J., Dougan, G., Mungall, K.L., Bentley, S.D., Holden, M.T.G., Wain, J., Churcher, C., Mungall, K.L., Bentley, S.D., Holden, M.T.G., Sebalhia, M., Baker, S., Basham, D., Brooks, K., Chillingworth, T., Connerton, P., Cronin, A., Davis, P., Davises, R.M., Dowd, L., White, N., Farrar, J., Feltwell, T., Hamlin, N., Haque, A., Hien, T.T., Holroyd, S., Jagels, K., Krogh, A., Larsen, T.S., Leather, S., Moule, S., O'Gaora, P., Parry, C., Quail, M., Rutherford, K., Simmonds, M., Skelton, J., Stevens, K., Whitehead, S. and Barrell, B.G.
Complete genome sequence of a multiple drug resistant Salmonella enterica seroyar Typhi CT18
                                                                                                                                                                                                                                                                                                                             Salmonella enterica subsp. enterica serovar Typhi.
Salmonella enterica subsp. enterica serovar Typhi
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Salmonella enterica serovar Typhi (Salmonella typhi) strain CT18
                                                                                                                                                                                                                                                                                                                                                                                                             AL513383.1 GI:16505740
                                                                                                                                                                                                                                                                                                                                                                                                                                                  plasmid pHCM1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STYPPHCM1
  Direct Submission
                  Parkhill, J.
                                                                                                                                                                                                                                                                                                               Salmonella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity
                                                                             Nature 413 (6858),
                                                         11677608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (bases 1 to 218160)
                                    (bases 1 to 218160)
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LRRGCEGHGIRLDYRPLGQPHYGGIVERIIGTAMQMIHDELPGTTFSNPDQRGDYDSE
NKAALTLRELERWLTLAVGTYHGSVHNGLLQPPAARWAEAVARVGVPAVVTRATSFLV
DFLPILRRTLTRTGFVIDHIHYYADALKPWIARRERWPSFLIRRDPRDISRIWVLEPE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RDLQGVGGEPPAVTAPLEQVQIDHTVIDLIVVDDRDRQPIGRPYLTLAIDVFTRCVLG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               join(7370. .7397,9012. .11455)
/insertion_seq="IS1326"
7370. .7395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATRKARRDADRRQHLKTSARPDKPVPPDTDIADPQADNLPPAKPFDQIEEW"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GQHYLEIPYRTLSHPAVTLWEQRQALAKLRQQGREQVDESALFRMIGQMREIVTSAQK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="tniBdeltal"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /gene="
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CCSLLASFAASLPLRRPSPIATLDMARYLLTRSEGTIGELAHLLMAAAIVAVESGEEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        note="100% identical to gp:TTU42226_7 [TniBdeltal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        INHRTLSMAC"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         51.2%;
96.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 miBdeltal"
                                                                             848-852 (2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 164.4; DB 1
pred. No. 2.5e-26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             218160 bp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 94281;
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FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Details of S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hinxton,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (25-OCT-2001) Submitted on behalf of the Salmonalla sequencing team, Sanger Centre, Wellcome Trust Genome Campus,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                http://www.sanger.ac.uk/Projects/S_typhi/).
Location/qualifiers
                                           /note="HCM1.04c"
complement(1876. .2346)
/gene="insB"
                                                                                                                 /note="13 bp inverted repeat flanking IS1" complement(1876. .2346)
           /note="HCM1.04c, insB, possible IS1 transposase,
                                                                                                                                                                                                                 complement(1871. .2585)
                                                                                                                                                                                                                                                                                                            /product "hypothetical protein"
/protein_id="CAD09621.1"
/db_xref="GI:16505743"
/translation="MNKPLVSFAELSGNAINVARQSVIDMEMDATREKIGKARSLFHS
                                                                                                                                                                                                                                      /note="possible RBS"
                                                                                                                                                                                                                                                            complement(1697.
                                                                                                                                                                                                                                                                                            GIHRAVNGYPLIQSAANQLAVIKRLLGDTKYLDACITENLCMFSPEGYLYLFMQRRFI
                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement(1367. .1690)
/gene="HCMI.03c"
/note="HCMI.03c, hypothetical protein, len: 107 aa;
unknown function"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement(1367, .1690)
/gene="HCM1.03c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement(742. .1053)
/gene="HCM1.02c"
                                                                                                                                                                                                                                                                                                                                                                                                              /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /product="hypothetical protein"
/protein_id="CAD09620.1"
/db_xref="GI:16505742"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      complement(742, .1053)
/gene="HCM1.02c"
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/note="possible RBS"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             unknown
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="HCM1.01c, possible membrane protein, len: 185 aa; unknown function, contains hydrophobic, possible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene-"HCM1.01c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Cambridge CB10 1SA E-mail: parkhill@sanger.ac.uk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    translation="MMYPDITGVKMKLSQLEVGMTVWSLSRTKMGNTTIKTVTLHSVV/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="HCM1.02c, hypothetical protein, len: 103 aa;
.nknown function"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product="putative membrane protein"
/protein_id="CAD09619.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            membrane-spanning regions. Spans sequence end"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement(1..528)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="GI:16505741"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Salmonella enterica subsp. enterica serovar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /gene="HCM1.01c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db_xref="taxon:90370"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /strain="CT18"
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                                                    RBS
         gene
                                                                                               RBS
                                                                                                                                                                               misc_feature
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4004 . . 4007
/note="possible RBS"
4014 . . 4343
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/product="putative magnesium and cobalt transport protein"
/protein_id="CAD09624.1"
/db_xref="G1:16505746"
/ttanslation="MLSAFQLENNRLTRLEVEESQPLVNAYWIDLYEPDDDERLRLQS
ELGQSEATRREELEDIEASARFEEDDDGLHIHSFFFFEDAEDHAGNSTVAFTIRDGRLF
TLRERELPAFRLYRWRARSQSWYDGNAYELLLDLFETKIRQLADEIENIYSDLEQLSR
VIMEGHQGDEVDEALSTLABLEDIGWYVRLLADDFALNFLYRKARLPGQLEQARE
VIMEGHQGDEVDEALSTLABLEDIGWYVRLAUFLYNGARLFGQLEQARE
ILRDIESLLPHNESLFQKVNFLMQAAMGFINIEQNRIIKIFSVVSVVFLPPTLVASSY
GNNFEFMFBLKWRFGYPAAIIFMILAGLAPYLYFKRKNWL"
                  /note="Pfam match to entry PF01544 CorA, CorA-like Mg2+transporter protein, score 432.90, E-value 2.8e-126" complement (3653. 3656)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="HCM1.07c, corA, probable magnesium and cobalt transport protein, len: 316 aa; similar to many e.g. SW:CORA_ECOLI (EMBL.iL11042), corA, Escherichia coli magnesium and cobalt transport protein (316 aa), fasta scores; E(): 0, 99.1% identity in 316 aa overlap. Contains Pfam match to entry PF01544 CorA, CorA-like Mg2+transporter protein. Contains hydrophobic, possible
                                                                                                                                                                       complement(2697. .3584)
'note-"possible RBS"
                                                                                                                                          /gene="corA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   membrane-spanning regions"
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/gene="corx"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement(2472. .2495)
/gene="insA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement(2284. .2289)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              / translation= "MASVSISCPSCSATDGVVRNGKSTAGHQRYLCSHCRKTWQLQFTYTASQPGTHQKIIDMAMNGVGCRATARIMGVGLNTILRHLKNSGRSR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="HCM1.05c, insA, probable IS1 transposase, len: 91 aa; highly similar to many from Enterobacteriaceae e.g. SW:ISA1_ECOLI (EMBL:X52534), insA, Escherichia coli insertion element IS1 protein InsA (91 aa), fasta scores; E(): 0, 98.9% identity in 91 aa overlap. Contains ps00017 ATP/GTP-binding site motif A (P-loop). Contains probable helix-turn-helix motif at aa 67-88"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="possible translational frameshift site, that determined experimentally (EMBL:X52534)"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /codon_start=:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product="putative IS1 transposase"
/protein_id="CAD09623.1"
/db_xref="G1:16505745"
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QRWLFYAYDRLRKTVVAHVFGERTMATLGRLMSLLSPFDVVIWMTDGWPLYESRLKGK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    transl_table=11/
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/protein_id="CAD09622.1"
/db_xref="GI:16505744"
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                                                                                             FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                               VERSION
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Best Local :
                                                                                                                                                         AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                JOURNAL
                                                                                                                                                                                                                                                         TITLE
                                                                                                                                                                                                                                                                                                                                                      ORGANISM
                                                                                                                                   JOURNAL
                                                                                                                                                                                                                                                                             AUTHORS
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                                                                                                                                                                                                                              Osborn,A.M., Bruce,K.D., Strike,P. and Ritchie,D.A. Sequence Conservation between Regulatory Mercury Resistance Genes from Mercury Polluted and Pristine Environments
                                                                                                                                                                                                                                                                                                                                                    Alcaligenes faecalis
Alcaligenes faecalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                 A.faecalis (SE20MERR) merR gene for regulatory protein
                                                                                           Submitted (13-MAY-1994) Osborn A. M., University of Liverpool, Genetics and Microbiology, Liverpool, Merseyside, UK, L69 3BX Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                          merk; regulatory protein.
                                                                                                                                                                                                                                                                                                                                                                                                               Z33484.1 GI:607038
                                                                                                                                                         Direct Submission
                                                                                                                                                                                                              Unpublished
                                                                                                                                                                                                                                                                                                                   Alcaligenes.
                                                                                                                                                                                                                                                                                                                                    Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ACCCACTGCGAGGAGGCCAGCCAGCCTGGCCGAACACACAAGCTCAAGGACGTGCGCGGAGAAG 175186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ACACACTGCGAGGAGGCCAGCAGCCTGGCCGAACACAAGCTCAAGGACGTGCGCGAGAAG 63
                                                                                                                                                                                                (bases
                                                                                                                                                                                                                                                                                             (bases 1 to 516)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="HCM1.08"
4014. .4343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /product="hypothetical protein".
/protein_id="cAD09626.1"
/db_xref="G1:16505748"
/translation="MGHYDYTRTLRVQLYDASRFHDGATAEQAGELHTVAFSKPAIAD
DIQKIVDTTAEVLGKRYSVNVFSN"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement(4363. .4569)
/gene="HCM1.10c"
/note="HCM1.10c, hypothetical protein, len: 68 aa; unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   complement(4363. .4569)
/gene="HCM1.10c"
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/db_xref-"G1:16505747"
/tanslation="MAHQLLIGKGMITLNLKRIFLALTLLPLFAVAADDCALSDPTLT
/translation="MAHQLLIGKGMITLNLKRIFLALTLLPLFAVAADDCALSDPTLT
/translation="MAHQLLIGKGMITLNLKRIFLALTLLPLFAVAADDCALSDPTLT
/translation="MAHQLLIGKGMITLNLKRIFLALTLLPLFAVAANDGGILNLTVFDIK
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                    /organism="Alcaligenes faecalis"
/isolate="SE20"
/db_xref="taxon:511"
/clone="pSE20R1, pSE20R2"
                                                                                                                                                                                            1 to 516)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  51.2%;
96.6%;
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Pred. No. 2.3e-26;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         516 bp
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                                                                                                                                     FEATURES
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TITLE
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            -10_signal
                                         -35_signal
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                                                                                                                                                                                                                                                                                                                                       merR; regulatory protein.
Enterobacter aerogenes.
Enterobacter aerogenes
                                                                                                                                                                                                                                                              1 (bases 1 to 516)
Osborn, A.M., Bruce, K.D., Strike, P. and Ritchie, D.A.
Sequence Conservation between Regulatory Mercury Resistance Genes
                                                                                                                                                                                                                                                                                                                                                                                                                  E.aerogenes merR gene for regulatory protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      50.7%;
Similarity 96.0%;
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                                                                                                                                                Genetics and Microbiology, Liverpool, Merseyside, UK, L69 3BX
                                                                                                                                                                  Submitted (13-MAY-1994) Osborn A. M.,
                                                                                                                                                                                    Direct Submission
                                                                                                                                                                                               Osborn, A.M.
                                                                                                                                                                                                                              Unpublished
                                                                                                                                                                                                                                                                                                             Enterobacter
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RYGEADVVRVKFVKSAQRLGFSLDEIAELLRLDDGTHCEEASSLAEHKLKDVREKMAD
LARMETYLSELVCACHARKGNVSCPLIASLQGEGGLARSAMP"
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/trans1_table=11
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/protein_id="cAA83892.1"
/db_xref="GI.607039"
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                   complement(13..18)
/citation=[1]
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           complement(28. .33)
                                                                                      /organism="Enterobacter aerogenes"
/isolate="T238"
/citation=[1]
                                                                        /db_xref="taxon:548"
                                                                                                                                    ocation/Qualifiers
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Pred. No. 7.3e-26;
O: Mismatches 7;
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                                                                                                                                                                       University of Liverpool,
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TITLE
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Best Local Similarity
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                                                                                                                                                                                                                                                               Submitted (15-SEP-1998) School of Biological Sciences, University of Liverpool, Crown Street, Liverpool, Merseyside L69 7ZD, UK
                                                                                                                                                                                                                                                                                                                 2 (bases 1 to 333)
Bruce, K.D., Lilley, A.K. and Bailey, M.J.
                                                                                                                                                                                                                                                                                                                                                                                              1 (bases 1 to 333)
Bruce, K.D., Lilley, A.K. and Bailey, M.J.
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Pseudomonas putida
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Pseudomonas putida group 2 plasmid MerR (merR) gene,
AF092069
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Proteobacteria; gamma subdivision; Pseudomonadaceae;
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                                    complement(<1. .>333)
/gene="merR"
                                                                             recovered in a Pseudomonas strain which was introduced into the samples" complement(<1...>333)
                                                                                                                               /db_xref="taxon:303"
/db_xref="taxon:303"
/plasmid="group 2 plasmid"
/plasmid="group 2 plasmid"
/note="this plasmid is naturally-occuring but was
/note="regulatory protein (repressor/inducer)"
/codon_start=1
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RYGAADVTRYKFYKSAGRAGFSLDEIAELLRLDDGTHCEEASSLAEHKLQDVREKMAD
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a 138 c 169 g 106 t
                                                                      /gene="merk"
                                                                                                                                                                                                   /strain="KT2440"
                                                                                                                                                                                                                /organism="Pseudomonas putida"
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72. .506
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/protein_id="CAA83896.1"
/db_xref="GI:607072"
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/citation=[1]
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/transl_table=11
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/citation=[1]
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89.7%;
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               124 CGAAAGGGGAATGTTTCCTGCCCGTTGATCGCGTCACTACAGG 166
                                                                    105 ATGGCCGACCTGGCGCGCATGGAAACCGTGCTGTCTGAACTGGTGTGCGCCTGCCATGCG 46
                                                                                                                                         165 ACCCACTGCGAGGAAGCCAGCAGCCTGGCCGAGCACAAGCTTCAGGACGTGCGCGAAAAG 106
                                                                                                     64 ATGGCCGACTTGGCGCGCATGGAAACCGTGCTGTCTGAACTCGTGTGCGCCTGCCATGCA 123
45 CGGAAGGGGAATGTTTCCTGCCCGCTGATTGAGTCGCTACAGG
                                                                                                                                                            4 ACACACTGCGAGGAGGCCAGCCCTGGCCGAACACAAGCTCAAGGACGTGCGCGAGAAG 63
                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                 67
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                                                                                                                                                                                                                                                                                                                                                           /protein_id="AAD52705.1"
/db_xref="GI:5817324"
/translation="IRFYQRKGLVPGPEQPYGSIPRYGAADVTRLRFYKSAQRLGFSL
                                                                                                                                                                                                                                                                                                                                                                                                                        /product="MerR"
                                                                                                                                                                                                                                                                                                                                                                                                                                          /transl_table=11
                                                                                                                                                                                                                                                                                                               109 c
                                                                                                                                                                                                                                       43.8%;
91.4%;
                                                                                                                                                                                                                  Score 140.6; DB 1;
Pred. No. 5.2e-21;
0; Mismatches 14;
                                                                                                                                                                                                                                                                                                             94 g
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Job time : 1800 secs Search completed: June 2, 2003, 06:52:54

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Maximum Match 100%
Listing first 45 summaries
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                   Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        June 2, 2003, 04:50:18; Search time 199 Seconds
                                                                               2185239 seqs, 1125999159 residues
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Copyright (c) 1993 - 2003 Compugen Ltd.
                                                                        /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2002.DAT:*
SUMMARIES
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3632.620 Million cell updates/sec
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				: 6		Description
ם	321	100.0	321	24	ABK52207	DNA encoding sunth
2	321	100.0	354	24	ABK52212	DNA opposite Sale
ω	321	100.0	509	24	ABK52213	Addacent placed a
4	164.4	51.2	435	24	ABK52206	DNA encoding ships
· U	164.4	51.2	7076	13	AAQ20186	HlvA gene with ctv
6	164.4	51.2	7076	16	AAQ86906	Vibrio cholerae di
7	129.2	40.2	568	15	AAQ58554	Mercury registant
œ	43.6	13.6	3012	21	AAZ52054	Codon ontimised up
9	43.6	13.6	8908	21	AAZ52055	Packaging construc

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	10.6	•	10.6	7	. 7	10.7	10.8	•	•	•		•	٠				11.3							12.8											
3111	2625	2598	930	4411529	4403765	378	24187	2215	1933	10732	1431	2963	902	3382	3382	2799	4319	3519	4343	4341	9788	12411	9792	9785	9783	9782	9407	9194	9194	9189	9170	9169	9167	9166	7897
22	22	22	21	22	22	24	23	24	24	21	23	23	23	14	13	19	21	16	24	24	24	24	24	24	24	24	24	24	24	24	24	24	24	24	24
AAD06236	AAD06237	AAD06235	AAC68143	AAI99682	AAI99683	ABQ91799	AAS59529	ABK47638	ABK47635	AAA10594	AAS54175	ABL02086	ABL02087	AAQ48249	AAQ29515	AAV49431	AAA70414	AAQ94352	AAI67896	AAI67897	ABK91622	ABK91613	ABK91618	ABK91624	ABK91620	ABK91621	ABK91623	ABK91612	ABK91611	ABK91607	ABK91614	ABK91617	ABK91619	ABK91616	ABK91609
mite	Domestic mite Bt11	Domestic mite Bt11	HIV-1 integrase ge	Mycobacterium tube	Mycobacterium tube	M. Capsulatus dene	Propionibacterium	cDNA encoding huma	-catenin	Gene encoding a su	Pseudomonas aerugi	Drosophila melanog				Bovine herpesvirus	HIV Gag-polymerase	BHV1 gI glycoprote	Nucleotide sequenc	de se	VΙΗ	VIΗ	ied HIV	VIH	ied HIV	ied HTV	VIH	YIH.	VIH	ied HIV	VIH	VIH	d HIV	ified HIV	Modified HIV prote

ALIGNMENTS

RESULT 1 ABK52207

DNA encoding synthetic MerR chelon variant.

13-AUG-2002 (first entry)

ABK52207;

ABK52207 standard; DNA; 321 BP.

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Mercuric ion; contaminated soil; ground water; hydroponic solution; irrigation water; waste stream; contaminated aqueous medium; biological fluid; gastrointestinal tract; chelon protein; enteric bacteria; toxic metal ion; mercury; cadmium; divalent cation; heavy metal binding protein; MerR; gene; ds.
12-OCT-2001; 2001WO-US31819.
                         18-APR-2002.
                                                  WO200230962-A2
                                                                                                                                                                                      Synthetic.
                                                                   /product= "Synthetic MerR chelon variant"
/note= "This sequence encodes the first 107 amino acids
of the synthetic MerR chelon variant. This
sequence lacks a stop codon"
                                                                                                                         /partial
                                                                                                                                                             Location/Qualifiers
                                                                                                                                    /*tag= a
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cc recombinant DNA molecule comprising a sequence encoding a chelon protein
CC which binds mercuric ions. The invention is useful for recombinantly
CC producing a protein in a host-cell, by infecting or transforming a host
CC cell capable of expressing a chelon coding sequence with a vector
CC comprising a promoter active in the host cell operably linked to a coding
CC region for the protein to produce a recombinant host cell and culturing
CC divalent mercuric ions, to take up, sequester and concentrate the heavy
CC immobilised onto a solid support, is useful for binding
CC inmobilised onto a solid support, is useful for concentrate the heavy
CC aqueous medium including biological fluids. The nucleic acid, when
CC recombinantly expressed in enteric bacteria (which are nontoxigenic and
CC compathogenic), is suitable for use in the in vivo sequestration and
CC climination of mercuric ion from gastrointestinal tracts of animals or
CC humans exposed to toxic metal ions such as mercury and/or cadmium. The
CC molecules of the invention are also useful in water treatment resins.
CC tation such as mercury or cadmium with high affinity. The present nucleic
CC acid sequence encodes the synthetic MerR chelon variant protein of the
CC threated chelons of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Novel non-naturally occurring recombinant DNA molecule encoding a chelon protein useful for binding divalent cation mercury from contaminated soil, water, aqueous medium including biological fluids -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12-OCT-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 321 BP; 72 A; 94 C; 103 G; 52 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present invention relates to a new non-naturally occurring
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 21; 42pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (UYGE-) UNIV GEORGIA RES FOUND INC.
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                                301
                                                                     241
                                                                                                                                                                                                                      121
                                                                                                                                                                                                                                                       121 GCACGAAAGGGGAATGTTTCCTGCCCGTTGATCGCGTCACTACAGGGATCCTCAGGCACC 180
                                                                                                                                            181
                                                                                                                                                                               181
                                                                                                                                                                                                                                                                                                                                                                                                                                            321;
                                                                                                                                                                                                                                                                                             61 AAGATGGCCGACTTGGCGCGCATGGAAACCGTGCTGTCTGAACTCGTGTGCGCCTGCCAT
                                                                                                                                                                                                                                                                                                                                                                                      1 ATGACACACTGCGAGGAGGCCAGCCAGCCTGGCCGAACACAAGCTCAAGGACGTGCGCGAG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                      GCCGACTTGGCGCGCATGGAAACCGTGCTGTCTGAACTCGTGTGCGCCTGCCATGCACGA 300
                                                                                                                                                                                                                                                                                                                                                                   ATGACACACTGCGAGGAGGCCAGCAGCCTGGCCGAACACAAGCTCAAGGACGTGCGCGAG
               AAGGGGAATGTTTCCTGCCCG 321
                                                                     CACTGCGAGGAGGCCAGCCTGGCCGAACACAAGCTCAAGGACGTGCGCGAGAAGATG
                                                                                                                                                                                                                    AAGATGGCCGACTTGGCGCGCATGGAAACCGTGCTGTCTGAACTCGTGTGCGCCTGCCAT
AAGGGGAATGTTTCCTGCCCG
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 321; DB 24; Length 321; 100.0%; Pred. No. 2e-77;
                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                0;
                                                                                                                                                                                                                            180
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1 ATGACACACTGCGAGGAGGCCAGCAGCCTGGCCGAACACAAGCTCAAGGACGTGCGCGAG 1 ATGACACACTGCGAGGAGGCCAGCAGCCTGGCCGAACACACAAGCTCAAGGACGTGCGCGAG

60

Query Match Best Local Matches

Similarity

100.0%;

Score 321; DB 24 Pred. No. 2.1e-77 Mismatches

DB 24;

Length 354; Indels

0,

Gaps

Conservative

0

Sequence 354 BP; 83 A; 103 C; 111 G; 57 T; 0 other;

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RESULT 2
ABK52212
irrigation water; waste stream; contaminated aqueous medium; biological fluid; gastrointestinal tract; chelon protein; enteric bacteria; toxic metal ion; mercury; cadmium; divalent cation; heavy metal binding protein; PCR; pASK-MBD; gene; ds.
                                                                                                                                        divalent mercuric ions, to take up, sequester and concentrate the heavy metal ions from contaminated soil, ground water, hydroponic solutions or irrigation water of waste streams. The DNA of the invention, when immobilised onto a solid support, is useful for concentrating heavy metal ions from contaminated environment waste streams or contaminated and recombinantly expressed in enteric bacteria (which are nontoxigenic and nonpathogenic), is suitable for use in the in vivo sequestration and elimination of mercuric ion from gastrointestinal tracts of animals or humans exposed to toxic metal ions such as mercury and/or cadmium. The molecules of the invention are also useful in water treatment resins. The nucleic acid of the invention is highly specific and binds divalent cation such as mercury or cadmium with high affinity. The present nucleic cation such as mercury and/or cadmium the nucleic cation such as mercury or cadmium with high affinity. The present nucleic cation such as mercury or cadmium with high affinity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cell capable of expressing a chelon coding sequence with a vector comprising a promoter active in the host cell operably linked to a coding region for the protein to produce a recombinant host cell and culturing the recombinant host cell under conditions, where DNA is expressed. The nucleic acid encoding the chelon protein is useful for binding the chelon protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABK52212 standard; DNA; 354 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 The present invention relates to a new non-naturally occurring recombinant DNA molecule comprising a sequence encoding a chelon protein which binds mercuric ions. The invention is useful for recombinantly producing a protein in a host-cell, by infecting or transforming a host
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Novel non-naturally occurring recombinant DNA molecule encoding a chelon protein useful for binding divalent cation mercury from contaminated soil, water, aqueous medium including biological fluids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12-OCT-2001; 2001WO-US31819
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (UYGE-) UNIV GEORGIA RES FOUND INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 24; 42pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Summers AO,
                                                                                                                 sequence represents the pASK-MBD gene, as described in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Caguiat JJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              contaminated soil; ground water; hydroponic solution;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          to a coding
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RESULT 3
ABK52213
ID ABK52213
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recombinant DNA molecule comprising a sequence encoding a chelon protein which binds mercuric ions. The invention is useful for recombinantly producing a protein in a host-cell, by infecting or transforming a host cell capable of expressing a chelon coding sequence with a vector comprising a promoter active in the host cell operably linked to a coding region for the protein to produce a recombinant host cell and culturing the recombinant host cell under conditions, where DNA is expressed.
                                                                                                                                                                                                                                                                                                                                            Novel non-naturally occurring recombinant DNA molecule encoding a chelon protein useful for binding divalent cation mercury from contaminated soil, water, aqueous medium including biological fluids
                                                                                                                                                                                                                           The present invention relates to a new non-naturally occurring
                                                                                                                                                                                                                                                                                               Disclosure; Page 25; 42pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P-PSDB; AAU97552.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Summers AO,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12-OCT-2000; 2000US-240465P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mercuric ion; contaminated soil; ground water; hydroponic solution; irrigation water; waste stream; contaminated aqueous medium; biological fluid; gastrointestinal tract; chelon protein; enteric bacteria; toxic metal ion; mercury; cadmium; divalent cation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Adjacent plasmid region encoding variant MerR protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           13-AUG-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABK52213;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               heavy metal binding protein; MerR; gene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ABK52213 standard; DNA; 509 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2002-435437/46.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAGGGGAATGTTTCCTGCCCG 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CACTGCGAGGAGGCCAGCCTGGCCGAACACAGCTCAAGGACGTGCGCGAGAAGATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAGGGGAATGTTTCCTGCCCG 321
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Caguiat JJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product= "Variant MerR protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ^{\mathrm{ds}}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           300
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RESULT 4
ABK52206
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CC The nucleic acid encoding the chelon protein is useful for binding CC divalent mercuric ions, to take up, sequester and concentrate the heavy CC metal ions from contaminated soil, ground water, hydroponic solutions or CC irrigation water of waste streams. The DNA of the invention, when CC immobilised onto a solid support, is useful for concentrating heavy metal contaminated environment waste streams or contaminated CC aqueous medium including biological fluids. The nucleic caid, when CC recombinantly expressed in enteric bacteria (which are nontoxigenic and CC nonpathogenic), is suitable for use in the in vivo sequestration and CC elimination of mercuric ion from gastrointestinal tracts of animals or CC molecules of the invention are also useful in water treatment resins. CC The nucleic acid of the invention is highly specific and binds divalent CC cacid represents the adjacent plasmid region that encodes the variant Merr cacid contain of the invention is highly specific and binds divalent CC acid represents the adjacent plasmid region that encodes the variant Merr contains of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Matches 321;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
                                                                                                                                                                                   Mercuric ion; contaminated soil; ground water; hydroponic solution; irrigation water; waste stream; contaminated aqueous medium; biological fluid; gastrointestinal tract; chelon protein; enteric bacteria; toxic metal ion; mercury; cadmium; divalent cation; heavy metal binding protein; MerR; gene; ds.
                                                                                                                                                             Shigella flexneri.
                                                                                                                                                                                                                                                                                                                 DNA encoding Shigella flexneri wild-type MerR protein.
                                                                                                                                                                                                                                                                                                                                                                   13-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                               ABK52206;
                                                                                                                                                                                                                                                                                                                                                                                                                                                ABK52206 standard; DNA; 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 509 BP; 139 A; 128 C; 140 G; 102 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       438 AAGGGGAATGTTTCCTGCCCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       241 GCCGACTTGGCGCGCATGGAAACCGTGCTGTGTGTAACTCGTGTGCGCCTGCCATGCACGA 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     181 CACTECGAGGAGGCCAGCCTGGCCGAACACACAAGCTCAAGGACGTGCGCGAGAAGATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              301 AAGGGGAATGTTTCCTGCCCG 321
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               198 AAGATGGCCGACTTGGCGCGCATGGAAACCGTGCTGTCTGAACTCGTGTGCGCCTGCCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              138 ATGACACTGCGAGGAGGCCAGCCAGCCTGGCCGAACACAAGCTCAAGGACGTGCGCGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       61 AAGATGGCCGACTTGGCGCGCATGGAAACCGTGCTGTCTGAACTCGTGTGCGCCTGCCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1 ATGACACACTGCGAGGAGGCCAGCAGCCTGGCCGAACACAAGCTCAAGGACGTGCGCGAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GCCGACTTGGCGCGCATGGAAACCGTGCTGTCTGAACTCGTGTGCGCCTGCCATGCACGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CACTGCGAGGAGGCCAGCCAGCCTGGCCGAACACACAAGCTCAAGGACGTGCGCGAGAAGATG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                 Location/Qualifiers
                                         /product= "Shigella flexneri wild-type MerR protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 321; DB 24; Length 509;
Pred. No. 2.2e-77;
); Mismatches 0; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   437
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WO200230962-A2

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cc producing a protein in a host-cell, by infecting or transforming a host cell capable of expressing a chelon coding sequence with a vector cc comprising a promoter active in the host cell operably linked to a coding cregion for the protein to produce a recombinant host cell and culturing cc region for the protein to produce a recombinant host cell under conditions, where DNA is expressed. Cc The nucleic acid encoding the chelon protein is useful for binding cc divalent mercuric ions, to take up, sequester and concentrate the heavy cc irrigation water of waste streams. The DNA of the invention, when cc inspection water of waste streams. The DNA of the invention or cc immobilised onto a solid support, is useful for concentrating heavy metal cc inspection water of waste streams. The nucleic acid, when cc recombinantly expressed in enteric bacteria (which are nontoxigenic and cc recombinantly expressed in enteric bacteria (which are nontoxigenic and cc molecules of the invention are also useful in water treatment resins. The nucleic acid of the invention are also useful in water treatment resins. The nucleic acid of the invention are also useful in water treatment resins. The nucleic acid of the invention is highly specific and binds divalent cation such as mercury or cadmium with high affinity. The present nucleic acid of the singella flexneri wild-type Merk protein of the production of heavy metal binding proteins termed chelons.
                                                                                AAQ20186
ID AAQ2
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 BXGXAX
                                                                                                               RESULT 5
                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel non-naturally occurring recombinant DNA molecule encoding a chelon protein useful for binding divalent cation mercury from contaminated soil, water, aqueous medium including biological fluids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12-OCT-2000; 2000US-240465P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12-OCT-2001; 2001WO-US31819.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            18-APR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention relates to a new non-naturally occurring
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                P-PSDB; AAU97551
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 20; 42pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (UYGE-) UNIV GEORGIA RES FOUND INC.
                                                                                                                                                                                                                                                                                                                                                                                       Sequence 435 BP; 95 A; 113 C; 146 G; 81 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     recombinant DNA molecule comprising a sequence encoding a chelon protein which binds mercuric ions. The invention is useful for recombinantly
HlyA gene with ctxB and mer gene inserted
                             31-MAR-1992 (first entry)
                                                                                   AAQ20186 standard; DNA; 7076 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2002-435437/46.
                                                                                                                                                                                                                                                                            238
                                                                                                                                                                                     124 CGAAAGGGGAATGTTTCCTGCCCGTTGATCGCGTCACTACAGGGATCCTCAGGC 177
                                                                                                                                                                                                                  64 ATGGCCGACTTGGCGCGCATGGAAACCGTGCTGTCTGAACTCGTGTGCGCCTGCCATGCA 123
                                                                                                                                                                                                                                                                                                                                     168;
                                                                                                                                                                                                                                                                                                        4
                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                           ACCCACTGCGAGGAGGCCAGCAGCCTGGCCGAACACAAGCTCAAGGACGTGCGCGAGAAG
                                                                                                                                                                                                                                                                                           ACACACTGCGAGGAGGCCAGCAGCCTGGCCGAACAACATCTCAAGGACGTGCGCGAGAAG
                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                                                                  51.2%;
96.6%;
                                                                                                                                                                                                                                                                                                                                      0
                                                                                                                                                                                                                                                                                                                                     Score 164.4; DB 24; Length 435; Pred. No. 3.8e-35; O; Mismatches 6; Indels 0;
                                                                                                                                                                                                                                                                                                                                         0
                                                                                                                                                                                                                                                                                                                                         Gaps
                                                                                                                                                                                                                             357
                                                                                                                                                                                                                                                                                  297
                                                                                                                                                                                                                                                                                                                                           0;
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         AAQ86906
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Matches 168;
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Best Local 9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Vibrio cholerae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The sequence is that of the haemolysin (hlyA) gene with two genes inserted into it, the cholera toxin subunit B gene (ctxB) and a mercury resistance gene (mer). It is used in the creation of a vibrio cholerae strain that has have 100% efficacy in protecting humans against subsequent infection with a strain of a similar serotype and avoid undesirable side effects such as diarrhoea, nausea and cramping. Cultures of these strains may be used for prodm. of vaccines against cholera. It is unclear whether the mer gene sequence is that of the sense or anti-sense straind as neither appears to have a clear reading frame. See also AAQ20185.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1992-007465/01.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      05-JUN-1990;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  05-JUN-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12-DEC-1991.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO9118979-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New Vibrio cholerae strains - comprise restriction endonuclease fragment encoding toxin, used as vaccines against cholera
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (UYMA-) UNIV MARYLAND BALTI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 7076 BP; 1578 A; 1978 C; 1966 G; 1554 T; 0 other
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Fig 21; 83pp; English.
AAQ86906 standard; DNA; 7076 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
                                                                                                                                                                                                                                                                                                                           5604 ACCCACTGCGAGGAGCCCAGCAGCCGAGCAGCAGCTCAAGGACGTGCGCGAGAAG
                                                                                                                                                 124 CGAAAGGGGAATGTTTCCTGCCCGTTGATCGCGTCACTACAGGGATCCTCAGGC 177
                                                                                                                                                                                                                                                                         64 ATGGCCGACTTGGCGCGCATGGAAACCGTGCTGTCTGAACTCGTGTGCGCCTGCCATGCA 123
                                                                                                                                                                                                                                                                                                                                                                          4 ACACACTGCGAGGAGGCCAGCCTGGCCGAACACACCAAGCTCAAGGACGTGCGCGAGAAG
                                                                                                                                                                                                                          CGAAAGGGGAATGTTTCCTGCCCGTTGATCGCGTCACTACAGGGCGAAGCAGGC 5777
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Baudry-Maurelli B,
                                                                                                                                                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     91WO-US03812.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      90US-0533315
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /*tag= a
/note= "interrupted hlyA gene"
complement (1193..819)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5882..7076
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            5873..1602
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /*tag= b
/note= "inserted ctxB gene"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note= "inserted mer gene"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note- "resumption of hlyA gene"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            *tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    *tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                     51.2%; Score 164.4; DB 1 96.6%; Pred. No. 6.4e-35;

 Mismatches

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 13; Length 7076;
                                                                                                                                                                                                                                                                                                                                                                                                                                   6,
                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                     0
                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
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RESULT 7
AAQ58554
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                                                                                                                                                                                                                                                                                                          Matches 168;
                                                                                                                                                                                                                                                                                                                         Query Match
Best Local (
      Mercury resistant control gene merR(1).
                                                           AAQ58554;
                                                                                    AAQ58554 standard; DNA; 568 BP
                                                                                                                                                                                                                                                                                                                                                                                                                New avirulent Vibrio cholerae strains of a non-01 serogroup can be used in vaccines to protect against cholera caused by non-01 strains. The new strains are derived from the 0139 serotype and the DNA encoding mercury resistance and the cholera toxin B subunit are necessary as a strains are immunogenic, inducing a strong local immunity and the mercury resistance gene allows the vaccine strain to be identified without the use of antibiotics. The new strains do
                               16-SEP-1994 (first entry)
                                                                                                                                                                                                                                                                                                                                                    Sequence 7076 BP; 1578 A; 1975 C; 1968 G; 1555 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                       not revert to the cholera toxin positive phenotype. For treatm approx. 1 million organisms are taken orally, in aqueous NaHCO3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 11; Figure 21; 109pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New avirulent strains of Vibrio cholerae expressing toxin B sub:unit - are stable against reversion and useful in oral vaccines to induce local protective immunity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1995-161574/21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (UYMA-) UNIV MARYLAND BALTIMORE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Vibrio cholerae; avirulent; serogroup; immunogenic; vaccine; cholera; toxin; mercury resistance; cholera toxin B subunit;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Vibrio cholerae disrupted haemolysin gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              08-OCT-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          08-OCT-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  07-OCT-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            20-APR-1995
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31-MAR-1996 (first entry)
                                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                          5724 CGAAAGGGGAATGTTTCCTGCCCGTTGATCGCGTCACTACAGGGCGAAGCAGGC 5777
                                                                                                                                                                                             124 CGAAAGGGGAATGTTTCCTGCCCGTTGATCGCGTCACTACAGGGATCCTCAGGC 177
                                                                                                                                                                                                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Levine MM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           93US-0133438.
93US-0133439.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 94WO-US11424.
                                                                                                                                                                                                                                                                                                                51.2%;

    Mismatches

                                                                                                                                                                                                                                                                                                                  Score 164.4; DB 16; Length 7076; Pred. No. 6.4e-35;
                                                                                                                                                                                                                                                                                                  6; Indels
                                                                                                                                                                                                                                                                                                                                                                                                              The new strains
                                                                                                                                                                                                                                                                                                  0; Gaps
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                                                                                                AAZ52054
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                                                                                                                                                                                                                                                                                                                                                                                                           XX
TT
TT
                                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local Similarity 78.3%; Pred. No. 1.3e-25;
                                                                                                                                                                                                                                                                                                                                                          Matches
Codon optimised Human immunodeficiency virus pol coding region.
                                  18-JUL-2000
                                                          AAZ52054;
                                                                              AAZ52054 standard; DNA; 3012 BP
                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 568 BP; 130 A; 150 C; 164 G; 124 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                            The mercury resistance genes can be used as selectable markers when used to transform other bacteria.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Page 2; 26pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mercury resistant control gene merR and shuttle vector - for enhanced expression of mercury resistance marker in transformed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 1994-077131/10.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RBS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Thiobacillus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   P-PSDB; AAR49668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17-JAN-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11-JAN-1994.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         JP06000083-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (DOWA ) DOWA MINING CO LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (AKIT-) AKITA KEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -10_signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Resistance; mercury; selectable marker; Thiobacillus ferrooxidans; transformation; detection; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Thiobacillus ferrooxidans.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ·35_signal
                                                                                                                                                506 GGTGACCGAGCCACTTGC 523
                                                                                                                                                                                           446 CGAAAGGGGAACGTTTCCTGCCCGCTAATTGCGTCACTAAAAAATCGCGCAGCGTGTCCG 505
                                                                                                                                                                                                            124 CGAAAGGGGAATGTTTCCTGCCGGTTGATCGCGTCACTACAGGGATCCTCAGGCACCCAC 183
                                                                                                                                                                       184 TGCGAGGAGGCCAGCAGC 201
                                                                                                                                                                                                                                              386 ATGGCCGACTTGGCGCGCATGGAGGCCGTGCTGTCCGAGCTTGTGTGCGCCTGCCATGCG
                                                                                                                                                                                                                                                                                                155;
                                                                                                                                                                                                                                                             64 ATGGCCGACTTGGCGCGCATGGAAAACCGTGCTGTCTGAACTCGTGTGTGCGCCTGCCATGCA 123
                                                                                                                                                                                                                                                                                                                       4 ACACACTGCGAGGAGGCCAGCAGCCTGGCCGAACACAAGCTCAAGGACGTGCGCGAGAAG 63
                             (first entry)
                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              91JP-0018338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     91JP-0018338
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89..568
/*tag=
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46..51
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76..79
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                                                                                                                                                                                                                                                                                                                                                     0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                           DB 15; Length 568;
                                                                                                                                                                                                                                                                                                                                                    43; Indels
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                                                                                                                                                                                                                                                                                                                                                  Gaps
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HIV; gag; packaging cell line; lentivirus; retroviral vector particle;

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The patent discloses new packaging cell line for producing a viral cc accessory protein independent lentivirus, preferably cc human immunodeficiency virus (HTV), derived retroviral vector particles. The packaging cell line comprises a mammalian cell, a retroviral DNA cc comprising a coding sequence for a lentivirus, preferably HTV, gagpol, cc where the coding sequence has been mutagenised to improve expression of cc the viral gagpol proteins, a second retroviral nucleotide sequence comprising the coding sequence for a heterologous envelope protein and a cc third retroviral nucleotide sequence comprising a DNA sequence of cc interest and lentivirus, preferably HTV, cis-acting sequences required for packaging, reverse transcription and integration.

Cc The packaging cell lines and viral particles can be used for gene comprising the development with improved safety. They can also be used in the development and production of vaccines and biochemical reagents. The present sequence is a pol coding region of codon optimised HTV creating accounts and reduces the risk of recombination between the transfer company and reduces the risk of recombination between the transfer read-arms.
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                                                                                                                                                                                                                                                                                                 Query Match
Best Local S
                                                                                                                                                                                                                                                                                  Matches 115;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Human immunodeficiency virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            pol; gene therapy; gene replacement; vaccine; biochemical reagent;
codon optimisation; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gray JT, Mulligan RC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11-SEP-1998;
12-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   10-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23-MAR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 43; Fig 9; 62pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New packaging cell line for producing a viral accessory protein independent HIV derived retroviral vector particles, useful in therapy or gene replacement -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (CHIL-) CHILDRENS MEDICAL CENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      P-PSDB; AAY70602.
                                                                                                                                                                                                                                                                                                                                                               Sequence 3012 BP; 679 A; 1017 C; 892 G; 424 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                     vector and gagpol mRNA.
                                                                                                                                                                                                 2403 CGAGGTGATCCCCGCCGAGACCGGCCAGGAGACCGCCTACTTCCTGCTGAAGCTGGCCGG 2462
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2000-271455/23.
                                         2523 GAAGGCCGCCTGCTGGTGGGCCGGCATCAAGCAGGAGTTCGGCATCCCCTACAACCCCCA 2582
                                                                                                                                                         72 CTTGGCGCGCATGGAAACCGTGCTGTCTGAACTCGTGTGCGCCTGCCATGCACGAAAGGG 131
                                                                                                                                                                                                                                      12 CGAGGAGGCCAGCAGCCTGGCCGAACACAAGCTCAAGGACGTGCGCGAGAAGATGGCCGA 71
                                                                                                                                                                                                                                                                                                         Similarity
GGCCAGCAGCCTGGCCGAACACAAGCTCAAGGACGTGCGCGAGAAGATGGCCGA 245
                                                                            GAATGTTTCCTGCCCGTTGATCGCGTCACTACAGGGATCCTCAGGCACCCCACTGCGAGGA 191
                                                                                                                      CCGCTGGCCCGTGAAGACCGTGCACACCGACAACGGCTCCAACTTCACCTCCACCACCGT 2522
                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         98US-0100022.
98US-0100063.
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1..3012
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/product= "pol protein"
/partial
                                                                                                                                                                                                                                                                                                       13.6%;
                                                                                                                                                                                                                                                                                                     Score 43.6; DB 21; Length 3012; Pred. No. 0.022;
                                                                                                                                                                                                                                                                                      Mismatches
                                                                                                                                                                                                                                                                                        119;
                                                                                                                                                                                                                                                                                        Indels
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RESULT 9
AAZ52055
ID AAZ5
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AC AAZ5
XX
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                                                                                                                                                                                                                                                                                                                                                                                                                    misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                            mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     packaging
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                                                                                                                                                                                                                                                                                                                         misc_feature
                                                                                                                                                                                                       misc_feature
                                                                                                                                                                                                                                                                                         polyA_site
WPI; 2000-271455/23
                    Gray JT,
                                                               11-SEP-1998;
12-SEP-1998;
                                                                                               10-SEP-1999;
                                                                                                                   23-MAR-2000
                                                                                                                                         WO200015819-A1
                                                                                                                                                                                                                                      rep_origin
                                         (CHIL-) CHILDRENS MEDICAL CENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gag;
gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2583 GTCCCAGGCGTGATCGAGTCCATGAACAAGGAGGTGAAGAAGAATCATCGGCCA 2636
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    packaging cell line; lentivirus; retroviral vector particle; therapy; gene replacement; vaccine; biochemical reagent; construct; plasmid; pHDMHgpm2; cyclic; circular; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               construct pHDMHgpm2 DNA.
                     Mulligan RC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rhesus macaque polyoma virus.
Human immunodeficiency virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human cytomegalovirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens.
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                                                               98US-0100022.
98US-0100063.
                                                                                                                                                                                                                                                                                                                       /~tag= g
/product= "
5710..6469
                                                                                               99WO-US20675
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers 97..679
                                                                                                                                                             /*tag= l
/note= "This region consists of the gagpol overlap
and cis-acting signals necessary for translation of
pol which are not optimised"
                                                                                                                                                                                                                                      /*tag= j
/product= "beta-lactamase (bla)"
8796..8908
                                                                                                                                                                                                                                                                                                                                                                                                                       /*tag- d
761..1303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Tabel = CMV_enhancer/promoter
                                                                                                                                                                                                         2583..2819
                                                                                                                                                                                                                                                             6709..7569
/*tag= j
                                                                                                                                                                                                                                                                                           /label= Human_betaglobin_sequence
5897..5921
                                                                                                                                                                                                                                                                                                                                                          /product= "Codon
2613..5624
                                                                                                                                                                                                                 'label SV40_origin_of_replication
                                                                                                                                                                                                                                                                                                                                                                                        318..2820
                                                                                                                                                                                                                                                                                                                                                                                                   *tag= e
label= Human_betaglobin_sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               79..1254
                                                                                                                                                                                                                                                                                                                                                                                                                                          ..5921
                                                                                                                                                                                                                                                                                                                                   "Codon optimised pol"
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                                                                                                                                                                                                                                                                                                                                                                    optimised gag"
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RESULT 10
ABR9169
ID ABR9
XX ABR9
AC ABR9
XX ABR9
XX HIV,
KW Env,
KW Env,
KW acqu
OS Synt
XX WO2(
XX W
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CC accessory protein independent lentivirus, preferably
CC human immunodeficiency virus (HIV), derived retroviral vector particles.
CC The packaging cell line comprises a mammalian cell, a retroviral DNA
CC comprising a coding sequence for a lentivirus, preferably HIV, gagyol,
CC where the coding sequence has been mutagenised to improve expression of
CC the viral gagool proteins, a second retroviral nucleotide sequence
CC comprising the coding sequence for a heterologous envelope protein and a
CC third retroviral nucleotide sequence comprising a DNA sequence of
CC interest and lentivirus, preferably HIV, cis-acting sequences required
CC the packaging cell lines and viral particles can be used for gene
CC therapy or gene replacement with improved safety. They can also be used
CC the packaging cell lines and viral particles can be used for gene
CC therapy or gene replacement with improved safety. They can also be used
CC the production of that of a packaging construct phHMHgpm2 which
CC comprises a codon optimised HIV gagool. The plasmid is defective for the
CC production of the viral envelope and accessory proteins e.g. tat, vif,
CC vpr, rev and Rev response element (RRE). It also lacks the viral
CC sequences which are transcribed into mRNA, e.g. constitutive transport
CC cell line.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches 115;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                   25-APR-2002
                                                                                                                 WO200232943-A2
                                                                                                                                                                                                                                                                              HIV; human immunodeficiency virus; gene; ds; circular; cyclic; anti-HIV; Env; Gag; Pol; Nef; genetic immunisation; protein immunisation; AIDS;
                                                                                                                                                                                                                                                  acquired immunodeficiency syndrome; cytotoxic T lymphocyte; CTL
                                                                                                                                                                                                                                                                                                                                                                                                   Modified HIV protein-encoding plasmid DNA #161.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         14-AUG-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABK91609 standard; DNA; 7897
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 8908 BP; 2134 A; 2579 C; 2355 G; 1840 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Fig 10; 62pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The patent discloses new packaging cell line for producing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              therapy or gene replacement -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New packaging cell line for producing a viral accessory protein independent HIV derived retroviral vector particles, useful in gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P-PSDB; AAY70599, AAY70602.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5195 GTCCCAGGGCGTGATCGAGTCCATGAACAAGGAGCTGAAGAAGATCATCGGCCA 5248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                5135 GAAGGCCGCCTGCTGGTGGGCCGGCATCAAGCAGGAGTTCGGCATCCCCTACAACCCCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     5015
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          132 GAATGTTTCCTGCCCGTTGATCGCGTCACTACAGGGATCCTCAGGCACCCACTGCGAGGA 191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       72 CTTGGCGCGCATGGAAACCGTGCTGTCTGAACTCGTGTGCGCCTGCCATGCACGAAAGGG 131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GGCCAGCAGCCTGGCCGAACACAAGCTCAAGGACGTGCGCGAGAAGATGGCCGA 245
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CGAGGTGATCCCCGCCGAGACCGGCCAGGAGACCGCCTACTTCCTGCTGAAGCTGGCCGG 5074
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49.1%;
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Best Local
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                                                                                                                                                                                14-AUG-2002 (first entry)
                                                                                                                                                                                                                                                  ABK91616 standard; DNA;
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14-NOV-2000; 2000US-252115P.
28-MAR-2001; 2001US-279257P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    immunisation for acquired immunodeficiency syndrome or human immunodeficiency virus infection
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local Similarity
                                                                                                                                                                                                                                                                                                                                 4459 GAGCCAGGGCGTGATCGAGAGCATGAACAAGGAGCTGAAGAAGATCATCGGCCAGGTG 4516
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4339 CCGCTGGCCCGTGAAGACCGTGCACACCGACAACGGCAGCAACTTCACCAGCACCACCACCGT 4398
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                                                                                                                                                                                                                                                                                                                                                                                                                                 132 GAATGTTTCCTGCCCGTTGATCGCGTCACTACAGGGATCCTCAGGCACCCACTGCGAGGA 191
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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HIV; human immunodeficiency virus; gene; ds; circular; cyclic; anti-HIV; Env; Gag; Pol; Nef; genetic immunisation; protein immunisation; AIDS; acquired immunodeficiency syndrome; cytotoxic T lymphocyte; CTL.

Modified HIV protein-encoding plasmid DNA #168.

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RESULT 12
ABK91619
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Best Local
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14-NOV-2000; 2000US-252115P.
28-MAR-2001; 2001US-279257P.
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                                              HIV; human immunodeficiency virus; gene; ds; circular; cyclic; anti-HIV; Env; Gag; Pol; Nef; genetic immunisation; protein immunisation; AIDS; acquired immunodeficiency syndrome; cytotoxic T lymphocyte; CTL.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New modified human immunodeficiency virus Env, Gag, Pol of Nef DNA and its encoded protein, useful as vaccines for genetic or protein immunisation for acquired immunodeficiency syndrome or human immunodeficiency virus infection
                                                                                                                       Modified
                                                                                                                                                        14-AUG-2002
                                                                                                                                                                                              ABK91619
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5628 CCGCTGGCCCGTGAAGACCGTGCACACCGACAACGGCAGCAACTTCACCAGCACCACCGT 568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    5568 CGAGGTGATCCCCGCCGAGACCGGCCAGGAGACCGCCTACTTCCTGCTGAAGCTGGCCGG
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                                                                                                                 HIV protein-encoding plasmid DNA #171.
                                                                                                                                                                                                                                                                                                                                                      GGCCAGCAGCCTGGCCGAACACAAGCTCAAGGACGTGCGCGAGAAGATGGCCGACTTG
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14-NOV-2000;
28-MAR-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (human immunodeficiency virus) protein. The nucleic acid molecule and its encoded protein (modified HIV Env, Gag, Pol or Nef) are useful for genetic or protein immunisation to a host, respectively. In particular these are useful for ameliorating the symptoms of acquired immunodeficiency syndrome (AIDS) or HIV infection and generating an antibody or cytotoxic T lymphocyte (CTL) response against native HIV Env, Gag, Pol or Nef. Furthermore, the nucleic acids, proteins and subsequent compositions are useful for treating or preventing HIV infections or NESU1449-ABK91624 represent modified HIV protein-encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New modified human immunodeficiency virus Env, Gag, Pol of Nef DNA and its encoded protein, useful as vaccines for genetic or protein immunisation for acquired immunodeficiency syndrome or human immunodeficiency virus infection -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 9167 BP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     plasmid DNA sequences of the invention.
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                                                                                                                                                                                                                                                                                                                                                     5689
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                                                                                                                                                                                                                                                                                                                                                                                                                        CCGCTGGCCCGTGAAGACCGTGCACACCGACAACGGCAGCAACTTCACCAGCACCACCGT 5688
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2000US-252115P.
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HIV; human immunodeficiency virus; gene; ds; circular; cyclic; anti-HIV; Env; Gag; Pol; Nef; genetic immunisation; protein immunisation; AIDS; acquired immunodeficiency syndrome; cytotoxic T lymphocyte; CTL.

14-AUG-2002

(first entry)

Modified HIV

protein-encoding plasmid DNA #169.

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ABK91614
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Best Local :
HIV; human immunodeficiency virus; gene; ds; circular; cyclic; anti-HIV; Env; Gag; Pol; Nef; genetic immunisation; protein immunisation; AIDS;
                                                         Modified HIV protein-encoding plasmid DNA #166.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The invention relates to a nucleic acid molecule encoding a modified HIV (human immunodeficiency virus) protein. The nucleic acid molecule and its encoded protein (modified HIV Env, Gag, Pol or Nef) are useful for genetic or protein immunisation to a host, respectively. In particular these are useful for ameliorating the symptoms of acquired immunodeficiency syndrome (AIDS) or HIV infection and generating an antibody or cytotoxic T lymphocyte (CTI) response against native HIV Env, Gag, Pol or Nef. Furthermore, the nucleic acids, proteins and subsequent compositions are useful for treating or preventing HIV infections or LTDS. Sequences ABK91449-ABK91624 represent modified HIV protein-encoding plasmid DNA sequences of the invention.
                                                                                                    14 - AUG - 2002
                                                                                                                                         ABK91614;
                                                                                                                                                                    ABK91614 standard; DNA; 9170 BP
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14-NOV-2000;
28-MAR-2001;
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Best Local Similarity
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        Modified HIV protein-encoding plasmid DNA #159
                                                    14-AUG-2002
                                                                                          ABK91607;
                                                                                                                        ABK91607 standard; DNA; 9189 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (human immunodeficiency virus) protein. The nucleic acid molecule and its encoded protein (modified HIV Env. Gag. Pol or Nef) are useful for genetic or protein immunisation to a host, respectively. In particular these are useful for ameliorating the symptoms of acquired immunodeficiency syndrome (AIDS) or HIV infection and generating an antibody or cytotoxic T lymphocyte (CTL) response against native HIV Env. Gag. Pol or Nef. Furthermore, the nucleic acids, proteins and subsequent compositions are useful for treating or preventing HIV infections or AIDS. Sequences ABK91449-ABK91624 represent modified HIV protein-encoding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 9170 BP; 2225 A; 2669 C; 2519 G; 1757 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            plasmid DNA sequences of the invention.
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28-MAR-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to a nucleic acid molecule encoding a modified HIV (human immunodeficiency virus) protein. The nucleic acid molecule and its encoded protein (modified HIV Env. Gag. Pol or Nef) are useful for genetic or protein immunisation to a host, respectively. In particular these are useful for ameliorating the symptoms of acquired immunodeficiency syndrome (AIDS) or HIV infection and generating an antibody or cytotoxic T lymphocyte (CTL) response against native HIV Env. Gag. Pol or Nef. Furthermore, the nucleic acids, proteins and subsequent compositions are useful for treating or preventing HIV infections or AIDS. Sequences ABK91449-ABK91624 represent modified HIV protein-encoding plasmid DNA sequences of the invention.
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14-NOV-2000; 2000US-252115P.
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ALIGNMENTS

FEATURES Web : www.genoscope.cns.fr)

Determination of this BAC-end sequence was carried out as part of a collaboration with the European Drosophila Genome Project (EDGP). http://www.edgp.ebi.ac.uk...This Drosophila melanogaster BAC library (Dros BAC) was made by Alain Billaud at CEPH (Centre d'Etude du Polymorphisme Humain) with funding provided by a MRC project grant. The DNA was prepared from embryos by Alain Bucheton and Genevieve Payan. It has been constructed in the vector Drosophila melanogaster.
Drosophila melanogaster
Drosophila melanogaster
Elkaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
1 (bases 1 to 1101) fly), genomic survey sequence. AL108460 AL108460.1 GI:5628764 GSS. CNS017SY 1101 bp DNA linear GSS 26-JUL-1999 Drosophila melanogaster genome survey sequence SP6 end of BAC BACN37L08 of DrossBAC library from Drosophila melanogaster (fruit Submitted (23-JUL-1999) Genoscope - Centre National de Sequencage BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr Location/Qualifiers

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                                                                                                                                                                                                                                                                                                                                                        Tel: 61 62 465496
Fax: 61 62 465000
                                                                                                                                                                                                                                                                                                                                                                                                                              Div. of Plant Industry, CSIRO Canberra ACT 2601 AUSTRALIA
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                                                                                                                                                                                                                                                                          Email: rudi@pi.csiro.au
International Triticeae EST Cooperative (ITEC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Contact: Appels R
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/organism="Drosophila melanogaster"
/ob_xref="taxon:7227"
/clone="BACN37LO8"
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/plasmid="pBeloBAC11"
/note-"end : SP6"
176 c 160 g
/cultivar="Wyuna"
/db_xref="taxon:4565"
/clone="C58004H01"
/clone_lib="ITEC CSB Wheat Endosperm Library"
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                                                                                                                                            organism="Triticum aestivum"
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BRY_3391 wheat EST endosperm library Triticum aestivum cDNA 5',
mRNA sequence.
BQ607497
                                                                                                                                                                                                                                   The Arabidopsis Information Resource
Carnegie Institution of Washington, Del
260 Panama Street, Stanford, CA 94305,
Tel: 1 650 325 1521 x 251
Fax: 1 650 325 3748
                                                                                                                                                                                                                                                                                                                                               Interpreting wheat EST sequences Unpublished (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Triticum aestivum
                                                                                                                                                                                                                                                                                                                                                                                        Clarke, B., Lambrecht, M. and Rhee, S.
Assessing the utility of Arabidopsis genomic information for
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooldeae
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/dev_stage="8-12 days post anthesis"
/lab_host="Escherichia coli SOLR"
/note="Twector: Lambda Zap/Bluescript; Site_1: XhoI;
Site_2: EcoRI; Plants grown in Phytotron with 18c/13C
(day/night) 16 hour light. MI3 Reverse sequencing primer
used. 1.0 Kbp average insert size."
a 218 c 185 g 71 t
                 /organism="Triticum aestivum"
/cultivar="Wyuna"
                                                                                                      /clone_lib="wheat EST endosperm library"
                                                                                                                              /db_xref-"taxon:4565"
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Best Local Similarity
                                                                                                                                                                                                                                                 source
        64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      201 CCTGGCCGAACACAAGCTCAAGGACGTGCGCGAGAAGATGGCCGACTTGGCGCGCATGGA 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      141 CTGCCCGTTGATCGCGTCACTACAGGGATCCTCAGGCACCCACTGCGAGGAGGCCAGCAG 200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       332 GATGGAGGTCGACGGCGCGAGGACGAGGAGGTCGACGAGGTCGCCCAGGCCAAGGCCGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       120;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      81 CATGGAAACCGTGCTGTGTGAACTCGTGTGCGCCTGCCATGCACGAAAGGGGAATGTTTC 140
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       21 CAGCAGCCTGGCCGAACACAAGCTCAAGGACGTGCGCGAGAAGATGGCCGACTTGGCGCG 80
                                                                                                                                                                                                                                                                          Plate: 108 row: H column: 15
Seq primer: ATTTAGGTGACACTATAG.
                                                                                                                                                                                                                                                                                                                                                                         Single pass sequencing. Bases called and alt_trimmed with phred v0.989904.e. Vector identified by cross_match with the -minscore 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Smith TPL
USDA, ARS, US Meat Animal Research Center
PO Box 166, Clay Center, NE 68933-0166, USA
                                                                                                                                                                                                                                                                                                            BACKWARD: GTTTTCCCAGTCACGACG
                                                                                                                                                                                                                                                                                                                                FORWARD: AGGAAACAGCTATGACCAT
                                                                                                                                                                                                                                                                                                                                                  PCR PRimers
                                                                                                                                                                                                                                                                                                                                                                                                                                  Tel: 402 762 4366
Fax: 402 762 4390
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Design and use of two pooled tissue normalized cDNA libraries for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1 (bases 1 to 524)
Fahrenkrug.S.C., Freking,B.A., Rohrer,G.A., Smith,T.P.L., Casas,E fahrenkrug.S.C., Greking,B.A., Rohrer,G.A., Laegreid,W.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    pig.
Sus scrofa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BI341447 524 bp mRNA linear 368872 MARC 2PIG Sus scrofa cDNA 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                              Email: smith@email.marc.usda.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       BI341447.1 GI:15034736
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GCTCGCCGAGCTCAACATGGACGCCTACGACGAGGAGGAGGACGGGCTCGAGCTTTTCAG 511
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   discovery in swine
          Conservative
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                                                                                /note="Vector: pCMV SPORT6; Site_1: NotI; Site_2: SalI; Library made from pooled tissue from testis, ovary, endometrium, hypothalamus, pituitary, and placenta." a 180 c 165 g 95 t
                                                                                                                                                         /tissue_type="pooled"
/lab_host="DH10B"
                                                                                                                                                                                          /db_xref="taxon:9823"
/clone_lib="MARC 2PIG"
                                                                                                                                                                                                                            /organism="Sus scrofa"
                                                                                                                                                                                                                                                                Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Metazoa; Chordata; Craniata; Vertebrata;
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                       11.9%;
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        0,
                     Score 38.2; D
Pred. No. 5.5;
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                                   DB 13; Length 524;
     43;
     Indels
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                                                                                                                                                Local
                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     High quality sequence stop: 736
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Plate: 013 row: D column: 05
Seq primer: M13 reverse primer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       20247247
Other_GSSs: 013_p_05-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Class: BAC ends
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CNS sequencing ID=DG0AA013CB03BP1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Contact: Pierce RJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Schistosoma mansoni
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INSERM U 167
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                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1. .736
                                                                                                                                                                                                                                                                                                                                                                                                                     /db_xref="taxon:6183"
/clone="013D05"
                                                                                                                                                                                                                                                                                                                                                                                                                                                     /strain="Puerto-Rican"
                                                                                                                                                                                                                                                                                                                                                                                     /sex="mixed"
                                                                                                                                                                                                                                                                                                                                                                                                     /clone_lib="SmBAC1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Location/Qualifiers
                                                                                                                                              55.5%;
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Pred. No. 7;
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554 AGGCCAACGATGGCTGGGTGCATGGTGCAGCACTATTTCGCCAGCGCCTGGCTGCGCM 613
                                                                239 TGGCCGACTTGGCGCGCATGGAAACCGTGCTGTCTGAACTCGTGTGCGCCTGCCATGCAC 298
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11 GCGAGGAGGCCAGCAGCCTGGCCGAACAACCTCAAGGACGTGCGCGGAGAAGATGGCCG 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Institut Pasteur de Lille
1 rue du Professeur A. Calmette, 59019
Tel: (33) (0)3 20877783
Fax: (33) (0)3 20877888
Email: Raymond.Pierce@pasteur-lille.fr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Le Paslier,M.-C., Pierce,R.J., Merlin,F., Hirai,H., Wu,W., Williams,D.L., Johnston,D., LoVerde,P.T. and Le Paslier,D.
Construction and characterization of a Schistosoma mansoni bacterial artificial chromosome library
Genomics 65 (2), 87-94 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeidida; Schistosomatoidea; Schistosomatidae; Schistosoma. 1 (bases 1 to 736)
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013_D_05-rev SmBAC1 Schistosoma mansoni genomic clone 013D05 5',
                                                                                                                                                                                                                                                                                                                                                                                                                                       sizing-ligation-transformations. Average insert size ranges from 70-127 kb and genome coverage is 7.9-fold."

253 c 247 g 99 t 5 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /dev_stage="cercariae"
/lab_host="Blomphalaria glabrata"
/note="Vector: pBeloBAC 11; Site_1: Hind III; Partially
Hind III digested and size-selected S. mansoni cercarial
DNA was ligated into Hind III digested pBeloBAC 11 vector
and used to transform E. coli DH10B. The complete library
contains 23808 clones from 4 independent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Schistosoma mansoni"
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RESULT 6
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                                                                                                                                                                                                                                                      299 GAAAGGGG 306
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Submitted (05-OCT-2001) Genoscope - Centre National de Sequencage : Bp 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr )

- Web : www.genoscope.cns.fr)

- Partially Hind III digested and size-selected S. mansoni cercarial DNA was ligated into Hind III digested pBeloBAC II vector and used to transform E. coll DH10B. The complete library contains 23808 clones from 4 independent sizing-ligation-transformations. Average insert size ranges from 70-127 kb and genome coverage is 7.9-fold.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Le Paslier,M.C., Pierce,R.J., Merlin,F., Hirai,H., Wu,W., Williams,D.L., Johnston,D., LoVerde,P.T. and Le Paslier,D. Construction and characterization of a Schistosoma mansoni bacterial artificial chromosome library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Platyhelminthes; Trematoda; Digenea; Strigeidida; Schistosomatoidea; Schistosomatidae; Schistosoma. 1 (bases 1 to 736)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genomics 65 (2), 87-94 (2000)
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                                                         BE636656 716 bp mRNA linear EST 03-JAN-2002 rockefeller.0.321 Mastigamoeba balamuthi lambda ZAP II Library Mastigamoeba balamuthi cDNA similar to small heat shock protein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Genoscope
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BE636656
BE636656.1 GI:9919767
                                          mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                     TGGCCGACTTGGCGCGCATGGAAACCGTGCTGTCTGAACTCGTGTGCGCCCTGCCATGCAC 298
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone_lib="SmBAC1"
/note="end : T3"
253 c 247 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Schistosoma mansoni"
/strain="Puerto-Rican"
/db_xref="taxon:6183"
/clone="013CB03"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
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55.5%;

    Mismatches

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Pred. No. 7;
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RESULT 8
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             148 TTGATCGCGTCACTACAGGGATCCTCAGGCACCCACTGCGAGGAGGCCAGCAGCCTGGCC 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            277 CTGGACAACGACAAGGTGCTGCGCGTGCGCGGGAGAAGAAGCGCGACGACGAGGGCTAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         208 GAACACAAGCTCAAGGACGTGCGCGAGAAGATGGCCGACTTGGCGCGCATGGA 260
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  88 ACCGTGCTGTCTGAACTCGTGTGCGCCTGCCATGCACGAAAGGGGAATGTTTCCTGCCCG 147
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  111;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The analysis of 100 genes supports the grouping of three highly divergent amoebae: Dictyostelium, Entamoeba, and Mastigamoeba proc. Natl. Acad. Sci. U.S.A. 99 (3), 1414-1419 (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Bapteste, E., Brinkmann, H., Lee, J.A., Moore, D.V., Sensen, C.W., Gordon, P., Durufle, L., Gaasterland, T., Lopez, P., Muller, M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mastigamoeba balamuthi.
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1 (bases 1 to 716)
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                                                                                                                                                                                                                                                                                                                                                                                                  BE601964 710 bp mRNA linear EST 22-OCT-2001
HVSMEh0100J10f Hordeum vulgare 5-45 DAP spike EST library
HVSMEh01009 (5 to 45 DAP) Hordeum vulgare cDNA clone HVSMEh0100J10f,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The Rockefeller University
                                          i (bases 1 to 710)
Wing,R., Close,T.J., Kleinhofs,A., Wise,R., Begum,D., Frisch,D., Y., Henry,D., Palmer,M., Rambo,T., Simmons,J., Choi,D.W., Fenton,R.D., Close,S.J., Oates,R. and Main,D. Development of a genetically and physically anchored EST resource for barley genomics: Morex 5-45 DAP spike cDWA library Unpublished (2001)
                                                                                                                                                                                                                       Hordeum vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooldeae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Insert Length: 716
Contact: Wing RA
                  Unpublished (2001)
On Aug 21, 2000 this sequence version replaced gi:9859525
                                                                                                                                                                                                                                                                                                                                                                                    mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   230 York Avenue, New York, NY 10021, I
2mail: mmuller@rockvax.rockefeller.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     aboratory of Biochemical Parasitology
                                                                                                                                                                                                                                                                                           Hordeum vulgare.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CTGGCCGAACACAAGCTCAAGGACGTGCGCGAGAAGATGGCCGACTTGGCGCGCATGGAA 87
                                                                                                                                                                                                       Triticeae; Hordeum.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="taxon:108607"
/clone_lib="Mastigamoeba balamuthi lambda ZAP II Library"
/note="syn: Phreatamoeba balamuthi"
228 c 214 g 104 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /organism="Mastigamoeba balamuth1"
/strain="ATCC 30984"
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KEYWORDS
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     161 TACAGGGATCCTCAGGCACCCACTGCGAGGAGGCCAGCCTGGCCGAACACAAGCTCA 220
                                                                                                                                                                                                                                          156 ACCGCGTCGGCGA 168
                                                                                                                                                                                                                                                                                       281 TGTGCGCCTGCCA 293
                                                                                                                                                                                                                                                                                                                                                  221 AGGACGTGCGCGAGAAGATGGCCGACTTGGCGCGCATGGAAACCGTGCTGTCTGAACTCG 280
                                                                                                                                                                                                                                                                                                                                        96
                                                                                                                                                                                                                                                                                                                                                                                                           WHE2320_H06_P12ZS Wheat pre-anthesis spike cDNA library Triticum aestivum cDNA clone WHE2320_H06_P12, mRNA sequence.
                                     BF484898.1 GI:11568199
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: rwing@clemson.edu
Total hq bases = 229
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Tel: 864 656 7288 Fax: 864 656 4293
                                                                                                                                                                                                                                                                                                                      AGGACGAGGTGGCGAGCATGGACCGGCGCCCCGCTCCTCGACCTCGGGCCACCCGCTCCTCA 155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                156 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="Vector: lambdaZAP; Site_1: EcoR1; Site_2: Xho1; Plants were grown in the greenhouse at the University of California, Riverside (Fenton, SJ Close, TJ Close). Whole spikes with awns trimmed were collected at 5, 10, 15, 20, 30 and 45 DAP (Fenton). Total RNA was prepared from each pool, equal quantities of all six RNA pools were combined, unamplified cDNA library was made, and 1 million pfu were in vivo excised to give pBluescript SK(-) cDNA phagemids (Choi)in the TJ Close lab at the University of California, Riverside. Phagemids were plated and picked at the Clemson Prisch, Atkins and Wing). Plasmid DNA preparations, DNA sequencing and sequence analysis were performed at CUGI (Wing, Yu, Prisch, Henry, Simmons, Oates, Rambo, Main). The sequence has been trimmed to remove vector sequence above. For more details on library preparation and sequence analysis see of phred value 20 or sequence analysis see.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 sequence analysis see
http://www.genome.clemson.edu/projects/barley. To order
this clone see http://www.genome.clemson.edu/orders Also
see Close TJ. Wing R. Kleinhofs A. Wise R (2001)
Genetically and physically anchored EST resources for
barley genomics. Barley Genetics Newsletter 31:29-30.
(http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html)*

(http://wheat.pw.usda.gov/ggpages/bgn/31/cover.html)*
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/clone="HvsMth0100J10f"
/clone_Lib="Hordeum vulgare 5-45 DAP spike EST library
HvcDNA0009 (5 to 45 DAP)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /tissue_type="5-45 DAP Spike"
/lab_host="SOLR"
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Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                       279 ACGCCTTCGCCGGGCTGATGATCACGGCGGCGTTCCTGTCGGCCTGCGGCCTTCTGCGCCA 338
                                                                                                                                                                                                                                                                                                                                                                                                                               131 GGAATGTTTCCTGCCCGTTGATCGCGTCACTACAGGGATCCTCAGGCACCCACTGCGAGG 190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           159 GCCAGGGCAGCGGCGGCGGCGGCGACAAGGACAAGCCGGCGCGCGCGCGCGCGTCCT 218
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                71 ACTTGGCGCGCATGGAAACCGTGCTGTCTGAACTCGTGTGCGCCTGCCATGCACGAAAGG 130
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       11 GCGAGGAGGCCAGCCAGCCTGGCCGAACACAAGCTCAAGGACGTGCGCGAGAAGATGGCCG 70
                            WHE3563_G11_M21ZS Wheat developing grains cDNA library Triticum aestivum cDNA clone WHE3563_G11_M21, mRNA sequence.
BQ805185.1 GI:22029394
                                                                                                                      BQ805185
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticeae; Triticum.

1 (bases 1 to 479)

Anderson,O.D., Chao,S., Choi,D.W., Close,T.J., Fenton,R.D., Han, P.S., Hsia,C.C., Kang,Y., Lazo,G.R., Miller,R., Rausch,C.J., Seaton,C.L. and Tong,J.C.

The structure and function of the expressed portion of the wheat genomes - Pre-anthesis spike cDNA library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence have been trimmed to remove vector sequence and low quality sequence with phred score less than 20 seq primer: Stratagene SK primer.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               poly(A) RNA were prepared, a cDNA library was made, and the cDNA clones were in vivo excised to give pBluescript phagemids in the TJ Close lab (Choi, Close, Fenton) at the University of California, Riverside. Plasmid DNA preparations and DNA sequencing were performed in the OD Anderson lab (all other authors)."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="Vector: Lambda Uni-ZAP XR, excised phagemid; Site_1: ECORI; Site_2: XhoI; Plants were grown in the greenhouse. Whole spike with awns trimmed, white, gr and yellow anther were collected and total RNA, and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone_lib="Wheat pre-anthesis spike cDNA library"/tlssue_type="Spike before anthesis"/dev_stage="Adult plant"/leb_host="E. coli SOLR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /clone="WHE2320_H06_P12"
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Pred No. 12;
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REFERENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Altenbach, S., Anderson, O.D., Chao, S., Chin, A., Close, T.J., Cronin, K., Crossman, C., Fenton, R.D., Lazo, G.R., Pham, J., Rausch, C.J., Wilson, C. and Woo, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooldeae
; Triticeae; Triticum.
                                                                                                                                                   11 GCGAGGAGGCCAGCAGCCTGGCCGAACACAAGCTCAAGGACGTGCGCGAGAAGATGGCCG 70
                                                                                                                                                                                                                                      107;
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   71 ACTTGGCGCGCATGGAAACCGTGCTGTCTGAACTCGTGTGCGCCTGCCATGCACGAAAGG 130
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/clone_lib="Wheat developing grains cDNA library"
/tissue_type="whoie grains"
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/cultivar="Butte 86"
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180 c 197 g
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RESULT 11
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                  188 AGGAGGCCAGCAGCCTGGCCGAACACAAGCTCAAGGACGTGCGCGAGAAGATGGCCGACT 247
                                                          494 ATGTGGACGCCCTGCGCACGCCTCTTGCCCCCTACAGGGACCAACTTGCCCCAACGCTT 553
                                                                                                     128 AGGGGAATGTTTCCTGCCCGTTGATCGCGTCACTACAGGGATCCTCAGGCACCCACTGCG 187
                                                                                                                                                434 CCGAGCTGCAGGAGAAGCTGAGCCCACTGGGCGAGGAGATGCNCGANCGCCCGCGCGCCC 493
                                                                                                                                                                                                                                      AV651765 GLC Homo sapiens cDNA clone GLCCTC09 3', mRNA sequence.
                                                                                                                                                                                         68 CCGACTTGGCGCGCATGGAAACCGTGCTGTCTGAACTCGTGTGCGCCTGCCATGCACGAA 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Xu,X., Huang,J., Xú,Z., Qian,B., Zhu,Z., Yan,Q., Cai,T., Zhang,X., Xiao,H., Qu,J., Liu,F., Huang,Q., Cheng,Z., Li,N., Du,J., Hu,W., Shen,K., Lu,G., Fu,G., Zhong,M., Xu,S., Gu,W., Huang,W., Zhao,X., Hu,G., Gu,J., Chen,Z. and Han,Z.
Insight into hepatocellular carcinogenesis at transcriptome level insight into hepatocellular carcinogenesis.
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1 (bases 1 to 640)

Xu, X., Huang, J., Xu, Z., Qian, B., Zhu, Z., Yan, Q., Cai, T., Zhang, X.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               by comparing gene expression profiles of hepatocellular carcinoma with those of corresponding noncancerous liver proc. Natl. Acad. Sci. U.S.A. 98 (26), 15089-15094 (2001)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Email: hanzg@chgc.sh.cn
This clone is available at CHGC in Shanghai.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Chinese National Human Genome Center at Shanghai 351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai 201203, P. R. China Tel: 86-21-50801919(ex.45)
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/dev_stage="Adult"
/lab_host="SOLR"
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/clone_lib="GLC"
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                                                                                        253 CGCATGGAAACCGTGCTGTCTGA 275
                                                                                                                                                                                                     134 CAGCTGCGCGACGCGGTGCGCAAGTGGGTGGACAAAGCCTATGACTTCGAGCGCCGGCGC 193
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                                                                                                                                                                                                                                        133 AATGTTTCCTGCCCGTTGATCGCGTCACTACAGGGATCCTCAGGCACCCACTGCGAGGAG 192
                                                                                                                                                                                                                                                                                            74
                                                                                                                                                                                                                                                                                                                73 TTGGCGCGCATGGAAACCGTGCTGTCTGAACTCGTGTGCGCCTGCCATGCACGAAAGGGG 132
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  High quality sequence start: 22 High quality sequence stop: 304.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: asimpson@ludwig.org.br
This sequence was derived from the FAPESP/LICR Human Cancer Genome
Project. This entry can be seen in the following URL
(http://www.ludwig.org.br/scripts/gethtml2.pl?ti=IL3&t2=IL3-HT0059-
270899-010-H08&t3=1999-08-27&t4=1)
Seq.primer: puc 18 forward
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Tel: +55-11-2704922
Fax: +55-11-2707001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rua Prof. Antonio Prudente 109, 4 andar, 01509-010, Sao Paulo-Sp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The FAPESP/LICR Human Cancer Genome Project Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 (bases 1 to 304) HCGP http://www.ludwig.org.br/ORESTES.
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Ludwig Institute for Cancer Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Simpson A.J.G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                          CTCATGGGCCTGGCCGTGCCAGA 276
                                                                                                                           GCCATCGTCAAGGCGGGCGGCTACTCCAAGGAGGCCTGGGGCGAGATGGCTGAGCTGGGT 253
                                                                                                                                                               GCCAGCAGCCTGGCCGAACACACAAGCTCAAGGACGTGCGCGAGAAGATGGCCGACTTGGCG 252
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                                                                                                                                                                                                                                                                                                                                                                                                                                                              /note="organ: head_neck; Vector: puc18; Site_1: SmaI; Site_2: SmaI; A mini-library was made by cloning products derived from ORESTES PCR (U.S. Letters Patent application No. 196,716 - Ludwig Institute for Cancer Research) profiles into the pUC 18 vector. Reverse transcription of tissue mRNA and CDNA amplification were performed under Low stringency conditions."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /organism="Homo sapiens"
/db_xref="taxon:9606"
/clone_lib="HT0059"
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48.8%;
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EST.
Chlamydomonas reinhardtii.
Chlamydomonas reinhardtii
Chlamydomonas reinhardtii
Eukaryota, Viridiplantae; Chlorophyta; Chlorophyceae; Volvocales;
Chlamydomonadaceae; Chlamydomonas.
                                                                                                                                     707 bp mRNA linear EST 29-MAY-1024053G04.x1 C. reinhardtii CC-1690, normalized, Lambda Zap II Chlamydomonas reinhardtii cDNA, mRNA sequence.
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181 CGCGGGTGCAGGCGGGGGGAGCGCTGGCCCAGTGCTGCGGCATGCCG 227
                                                                                                                 121 CTCACCGGCAGTCTCCGCGCGCAGACGCGCGCCCTGTGCTCCAGGCCGTAGCAGTGCT 180
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                                                             219 CAAGGACGTGCGCGAGAAGATGGCCGACTTGGCGCGCATGGAAACCG 265
                                                                                                                                                                                                                                61 CGACATGTTCGCCGCTCCCGATGGCACCAAGCGACGTGCCAGCATCAAGCGGGACACGCT 120
                                                                                                                                                                                                                                                                                           99 TGAACTCGTGTGCGCCTGCCATGCACGAAAGGGGAATGTTTCCTGCCCGTTGATCGCGTC 158
                                                                                                                                                                                                                                                                                                                                                                                                          39 CAAGCTCAAGGACGTGCGCGAGAAGATGGCCGACTTGGCGCGCATGGAAACCGTGCTGTC 98
                                                                                                                                                                                                                                                                                                                                                        Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: asamizu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
Location/Qualifiers
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Generation of expressed sequence tags from low-CO2 and high-CO2 adapted cells of Chlamydomonas reinhardtii
DNA Res. 7 (5), 305-307 (2000)
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Contact: Erika Asamizu
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127 c 113 g 45 t
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/note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:
XhOI; The cDNA library was constructed from cells cultured
in a carbon stress acclimatized condition in which carbon
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Unpublished (2000)
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Durham, NC 27708-1000
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                                                                                                                                                                                              BM488564 linear EST 07-FEB-2 pgm2n. pk008.bl1 Normalized Chicken Breast Muscle, Leg Muscle, an Epiphyseal Growth Plate cDNA library (pgm2n) Gallus gallus CNA clone pgm2n.pk008.bl1 5' similar to gb|AAH09268.1|AAH09268 (BC009268) Similar to RIKEN CDNA B230113C15 gene [Homo sapiens],
Gallus gallus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Archosauria; Aves; Neognathae; Galliformes; Phasianidae;
                                                                                                                          BM488564
BM488564.1 GI:18609495
                                                                                                                                                                           mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (bases 1 to 707)
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919 613 8177
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/strain-"CC-1690 wild type mt+ 21gr"
/db_xref-"taxon:3055"
/clone_lib-"C. reinhardtii CC-1690, normalized, Lambda Zap
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note="Vector: pBluescript II SK-; Site_1: EcoRI; Site_2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 11.4%;
49.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             94;
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Search completed: June 2, 2003, 06:22:43 Job time: 1520 secs

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COMMENT
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TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           JOURNAL
                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                Query Match 11.3%;
Best Local Similarity 47.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  source
                                                                                  178 CAGTTGGCCCAGCAGTGGATCGACCGCATCCAGAGCTGCTTATCGGACGCCTGAGAGCCT
                                                                                                                                                                    118 ANAGCGTTCTTCGATCTGAAGACGACGAAACGCGTTTACAACTTCTGCGCCCAGGACGTG
                                         193 GCCAGCAGCCTGGCCGAACACAAGCTCAAGGACGTGCGCGAGAAGATGGCC 243
                                                                                                                           133 AATGTTTCCTGCCCGTTGATCGCGTCACTACAGGGATCCTCAGGCACCCACTGCGAGGAG 192
                                                                                                                                                                                                                                                                                                                                                109;
                                                                                                                                                                                                             73 TTGGCGCGCATGGAAACCGTGCTGTCTGAACTCGTGTGCGCCTGCCATGCACGAAAGGGG 132
                                                                                                                                                                                                                                                         58 GAGGTGGAGTCCATCACGCCCGGAACCCCCACCATGGGGGCCCCGGAAGACGGTGGACGAG 117
                                                                                                                                                                                                                                                                                                  13 GAGGAGGCCAGCAGCCTGGCCGAACACAAGCTCAAGGACGTGCGCGAGAAGATGGCCGAC 72
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Cogburn,L.A. and Monsonego-Ornan,E.
ESTs from Normalized Chicken Breast Muscle, Leg Muscle, and
Epiphyseal Growth Plate cDNA library, USDA/IFAFS Animal Genome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    University of Delaware Townsend Hall, Newark, DE 19717, USA Tel: 302-831-1335
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (2002)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Phasianinae; Gallus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Contact: Larry A.
CTCAGGGAGAGCCCCAACCCACGCACGGTCNTCTGCAGCGGAACAGAGCC 288
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (bases 1 to 480)
                                                                                                                                                                                                                                                                                                                                                                                                                                                           102 a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    302-831-2822
                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             cogburn@udel.edu, www.chickest.udel.edu.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="Vector: pCMVSPORT6; Library made from equivalent pools of total RNA isolated from each tissue (embryonic muscle 33.3%; Juvenile muscle 33.3%; and epiphyseal growth plate 33.3% of the final RNA pool). Single pass sequencing from 5'-end"

142 c 158 g 65 t 13 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           and Epiphyseal Growth Plate cDNA library (pgm2n)/sex="Male and Female"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Strains 90 & 21"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                growth plate"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /dev_stage="Breast,leg:Embryo(d19);post-hatch(1d,1,3,5,7,9,11 weeks);growth plate(1d,7d,14d post-hatch)"
/lab_host="E. coli_EMDH10B"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /strain="Commercial broiler and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    tissue_type="Breast muscle, leg muscle and epiphyseal/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone="pgm2n.pk008.b11"
/clone=lib="Normalized Chicken Breast Muscle, Leg Muscle,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ocation/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             organism="Gallus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cogburn
                                                                                                                                                                                                                                                                                                                                             0;
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Pred. No. 1
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                                                                                                                                                                                                                                                                                                                                                         0;
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QΥ
                                                                                                                                      The present invention describes primer sets for synthesising 5602 CC full-length cDNAs defined in the specification. Where a primer set CC comprises: (a) an oligo-dT primer and an oligonucleotide complementary strand of a polynucleotide which comprises one of CC the 5602 nucleotide sequences defined in the specification, where the CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination CC sequence and an oligonucleotide comprising a sequence complementary to the CC sequence and an oligonucleotide comprises a 3'-end sequence, where the CC oligonucleotide which comprises a 3'-end sequence, where the CC oligonucleotide which comprises a 3'-end sequence, where the CC oligonucleotide comprises a 3'-end sequence, where the CC the 5'-end sequence/3'-end sequence is selected from those defined in CC in gene therapy. The primers sets can be used in antisense therapy and comparticularly full-length cDNAs. The primers are useful for synthesising polynucleotides, and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length CDNAs. The primers allow obtaining of the full-length CDNAs easily without any specialised methods. AAH03166 to AAH13628 and CC AAB1563 to AAH13674 represent human cDNA sequences; and AAH13629 to AAH13620 of the present luman amino acid sequences; and AAH13629 to AAH13632 of the present human canno acid sequences; and AAH13629 to AAH13632 of the present invention.
                                            Matches
                                                              Query Match
Best Local
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AAH14532/c
                                                                                                      Sequence 4147 BP; 1078 A; 1016 C; 1118 G; 935 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 8; SEQ ID 12080; 2537pp + CD ROM; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       29-JUL-1999; 99JP-0248036.
27-AUG-1999; 99JP-0300253.
11-JAN-2000; 2000JP-0118776.
02-MAY-2000; 2000JP-0183767.
09-JUN-2000; 2000JP-0241899.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection and/or diagnosis of the abnormality of the proteins encoded by the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-318749/34.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   full-length cDNAs -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ishii S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (HELI-) HELIX RES INST.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EP1074617-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human; primer; detection; diagnosis; antisense therapy; gene therapy; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human cDNA sequence SEQ ID NO:12080
                                                            ocal
179 CCCACTGCGAGGAGGCCA 196
                                      18; Conservative
                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Isogai T, Nishikawa T, Hayashi K,
, Sugiyama T, Wakamatsu A, Nagai K
                            5.6%; Score 18; DB
100.0%; Pred. No. 13;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Nagai K,
                                                                  DB 22; Length 4147;
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K, Otsuki T;
                                  0; Indels
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Db 1159 CCCACTGCGAGGAGGCCA 1142
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Search completed: June 2, 2003, 08:39:1 Job time: 203 secs

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ABQ90147/c
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                                                                                                                                                                                                                                                                                                 Birkeland NK,
Lillehaug JR,
Salzberg SL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Micro array; gene; ds; differential expression; gene expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 1536 BP; 289 A; 500 C; 461 G; 286 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               M. capsulatus gene #132 for DNA array.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-OCT-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABQ90147;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ABQ90147 standard; DNA; 2595 BP
                                                                                                                                                     Novel DNA array useful for determining differential expression of Methylococcus capsulatus genes, comprises polynucleotides or oligonucleotides representative for a selective number of Methylococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200255655-A2.
                                                                                                                                                                                                                                                        WPI; 2002-557818/59.
                                                                                                                                                                                                                                                                                                                                                                                             (UNIF-) UNIFOB STIFTELSEN UNIV BERGEN. (TIGR-) TIGR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                12-JAN-2001; 2001NO-0000235.
12-JAN-2001; 2001NO-0000239.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    14-JAN-2002; 2002WO-NO00019
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 18-JUL-2002.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Methylococcus capsulatus
                                                                                      Claim 19; Page 115-116; 678pp; English.
                                                                                                                                  capsulatus genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              તે
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                                                                                                                                                                                                                                                                                                                           Lossius I,
                                                                                                                                                                                                                                                                                                               Eidhammer I, Journell JA,
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100.0%; Pred. No.
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isen JA, Fraser CM, Durkin AS;
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The invention relates to a novel DNA array giving a representation of a number of Methylococcus capsulatus genes. The method of the invention is useful for determination of the differential expression of the genes of

invention is he genes of

B δÃ

2956 CTGGCCGAACACAAGCTC 2973

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ABL23967
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                                Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  M. capsulatus, and for studying gene expression on a genomic scale and in gene expression assays of M. capsulatus genes. The sequences shown in ABQ90016-ABQ91855 represent M. capsulatus genes for use in arrays of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 2595 BP; 442 A; 737 C; 885 G; 531 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABL23967;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ABL23967 standard; DNA; 3873 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Drosophila melanogaster genomic polynucleotide SEQ ID NO 23374.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WO200171042-A2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Drosophila melanogaster
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           pharmaceutical; gene; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26-MAR-2002 (first entry)
                                                                                                                         The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly from WIPO at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                          insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins
                                                                                                                                                                                                                                             capable of detecting 1000 or more genes from Drosophila. The inventuation in developmental biology and in elucidating cell signalling cell-cell interactions in higher eukaryotes for the development of
                                                                                                                                                                                                                                                                                                                                Claim 1; SEQ ID NO 23374; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-656860/75.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Venter JC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23-MAR-2000; 2000US-191637P.
11-JUL-2000; 2000US-0614150.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23-MAR-2001; 2001WO-US09231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               27-SEP-2001.
                                                                                             Sequence 3873 BP; 998 A; 1083 C; 996 G; 796 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                           New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signalling and cell-cel
                                                                                                                                                                                                                                                                                             The invention relates to an isolated nucleic acid detection reagent
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (PEKE ) PE CORP NY.
                                                                                                                                                                                                                                                                                                                                                                 interactions
                                                                                                                                                                                (ABB57737-ABB72072)
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nes 18; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            429 CACAAGCTCAAGGACGTG 412
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28 CTGGCCGAACACAAGCTC 45
                                18;
                                                  Similarity
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                                Conservative
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                                                  100.0%;
                                                5.6%; Score 18; DB 23; Length 3873; 100.0%; Pred. No. 13;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Li PWD,
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                                    Mismatches
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01-DEC
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08-DEC
                                 (HUMA-) HUMAN GENOME SCI INC
                                                        08-DEC-2000;
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08-NOV-2000;
08-NOV-2000;
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20-OCT-2000;
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                       Barash SC,
                                            2001US-0259678.
                                                       2000US-0251990
                                                            2000US-0251989.
                                                                            2000US-0251856
                                                                                            2000US-02
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2000US-0237037.
2000US-0237038.
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2000US-0246474.
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2000US-0241809.
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2000US-0241785.
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                                                                                                                                                                                                                                                                                                                                             2000US-0240960.
                                                                                                                                                                                                                                                                                                                         2000US-0241787
                       Ruben SM;
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Nucleic acids encoding human immune/hematopoietic antigen polypeptides, useful for preventing, diagnosing and/or treating cancers and

WPI; 2001-483426/52.

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AAS82310/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ARK54951 to AAK64702 encode the human immune/haematopoietic antigen (I) amino acid sequences given in AAM62170 to AAM91921. (I) have cytostatic c activity, and can be used in gene therapy and vaccine production. (I) createns and polynucleotides may be used in the prevention, diagnosis and c treatment of diseases associated with inappropriate (I) expression. For c example, they may be used to treat disorders associated with decreased c expression by rectifying mutations or deletions in a patient's genome ct that affect the activity of (I) by expressing inactive proteins or to supplement the patients own production of (I). Additionally, (I) c polynucleotides may be used to produce the secreted (I), by inserting the nucleic acids into a host cell and culturing the cell to express the c protein. (I) proteins and polynucleotides may be used to prevent, c diagnose and treat immune/haematopoietic-related diseases, especially c ancers and cancer metastases of haematopoietic derived cells. ARK64703 c sequences from the present invention. ARK64942 to ARK84950 and AAM82169 crepresent sequences used in the exemplification of the present invention.
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Best Local (
The invention relates to isolated polynucleotide (I) and polypeptide (II) sequences. (I) is useful as hybridisation probes
                                                     Claim 1; SEQ ID No 18114; 103pp; English.
                                                                                          New isolated polynucleotide and encoded polypeptides, useful in diagnostics, forensics, gene mapping, identification of mutations responsible for genetic disorders or other traits and to assess biodiversity
                                                                                                                                                                                  P-PSDB; ABG18123.
                                                                                                                                                                                                 WPI; 2001-639362/73.
                                                                                                                                                                                                                                  Drmanac RT, Liu C,
                                                                                                                                                                                                                                                                     (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                    31-MAR-2000; 2000US-0540217.
23-AUG-2000; 2000US-0649167.
                                                                                                                                                                                                                                                                                                                                                      30-MAR-2001; 2001WO-US08631.
                                                                                                                                                                                                                                                                                                                                                                                                                              W0200175067-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; chromosome mapping; gene mapping; gene therapy; forensic; food supplement; medical imaging; diagnostic; genetic disorder; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DNA encoding novel human diagnostic protein #18114.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 13-FEB-2002 (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAS82310 standard; cDNA; 1536 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; SEQ ID NO 42287; 3071pp + Sequence Listing; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             5.6%; Score 18; 100.0%; Pred. No.
                                                                                                                                                                                                                                  Tang YT;
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RESULT 11
AAK8775
ID AAK877
XX AAK87
AC AAK87
XX O7-NO
DT 07-NO
XX Human
XX Human
XX Human
XX Homo
XX Homo
XX Homo
XX Homo
XX HOMO
OS HOMO
OS 17-JF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cy which binds mercuric ions. The invention is useful for recombinantly comprising a protein in a host cell, by infecting or transforming a host cell capable of expressing a chelon coding sequence with a vector comprising a promoter active in the host cell operably linked to a coding comprising a promoter active in the host cell operably linked to a coding region for the protein to produce a recombinant host cell and culturing companies. The nucleic acid encoding the chelon protein is useful for binding crimtopic contaminated soil, ground water, hydroponic solutions or crimtopic ions from contaminated soil, ground water, hydroponic solutions or constraint environment waste streams. The DNA of the invention, when conspication water of waste streams. The DNA of the invention and concentrated environment waste streams or contaminated concentrating heavy metal constraints and concentrating heavy metal constraints are contaminated environment waste streams or contaminated concentration and concentration of mercuric ion from gastrointestinal tracts of animals or elimination of mercuric ion from gastrointestinal tracts of animals or concentration and concentrate and concentration an
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                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
"~+~hes 19; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Novel non-naturally occurring recombinant DNA molecule encoding a chelon protein useful for binding divalent cation mercury from contaminated soil, water, aqueous medium including biological fluids -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (UYGE-) UNIV GEORGIA RES FOUND INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12-OCT-2000; 2000US-240465P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention relates to a new non-naturally occurring
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Page 24; 42pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     recombinant DNA molecule comprising a sequence encoding a chelon protein which binds mercuric ions. The invention is useful for recombinantly
                                                                                                                         Human; immune; haematopoletic; immune/haematopoletic antigen; cancer;
cytostatic; gene therapy; vaccine; metastasis; ds.
                                                                                                                                                                        Human immune/haematopoietic antigen genomic sequence SEQ ID NO:42287.
                                                                                                                                                                                                           07-NOV-2001 (first entry)
                                                                                                                                                                                                                                                                        AAK87475 standard; DNA; 1231 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 33 BP; 8 A; 8 C; 12 G; 5 T; 0 other;
17-JAN-2001; 2001WO-US01354.
                                                             WO200157182-A2.
                               09-AUG-2001.
                                                                                              Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                       15
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           07-JUN-2000;
28-JUN-2000;
30-JUN-2000;
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05-SEP-2000;
06-SEP-2000;
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14-SEP-2000;
14-SEP-2000;
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08-SEP-
12-SEP-
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01-SEP-2000
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14-SEP-2000;
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2000US-0180628.
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2000US-0216647.
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                                           2000US-0236368
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RESULT 9
AAQ58554
ID AAQ5
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AC AAQ5
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DT 16-S
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The present invention relates to a new non-naturally occurring crecombinant DNA molecule comprising a sequence encoding a chelon protein comprising a protein in a host-cell, by infecting or recombinantly created in a host-cell by infecting or transforming a host cell capable of expressing a chelon coding sequence with a vector comprising a promoter active in the host cell operably linked to a coding the recombinant host cell under conditions, where DNA is expressed. The nucleic acid encoding the chelon protein is useful for binding cell under conditions, where DNA is expressed. The nucleic acid encoding the chelon protein is useful for binding cell into strom contaminated soil, ground water, hydroponic solutions or immobilised onto a solid support, is useful for concentrate the heavy constitued in the contaminated contaminated contaminated environment waste streams or contaminated conspathogenic), is suitable for use in the in vivo sequestration and compathogenic), is suitable for use in the in vivo sequestration and contamination of mercuric ion from gastrointestinal tracts of animals or humans expressed to tryin marks increased environtestinal tracts of animals or contaminated contamination of mercuric ion from gastrointestinal tracts of animals or contaminated contamination of mercuric ion from gastrointestinal tracts of animals or contaminated contamination of mercuric ion from gastrointestinal tracts of animals or contaminated contamination of mercuric ion from gastrointestinal tracts of animals or contaminated contaminated contaminated contaminated contaminated contaminated contamination and contaminated contamination or marks in the in vivo sequestration and contaminated contamination contaminated 
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Best Local
                                       16-SEP-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                humans exposed to toxic metal ions such as mercury and/or cadmium. The molecules of the invention are also useful in water treatment resins. The nucleic acid of the invention is highly specific and binds divalent cation such as mercury or cadmium with high affinity. The present nucleic acid sequence represents synthetic product 2 forward PCR primer that was used in the methods of the invention for construction of pASK-MBD vector.
                                                                                                                                                                                                AAQ58554 standard; DNA; 568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 30 BP; 7 A; 11 C; 8 G; 4 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Novel non-naturally occurring recombinant DNA molecule encoding a chelon protein useful for binding divalent cation mercury from contaminated soil, water, aqueous medium including biological fluids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (UYGE-) UNIV GEORGIA RES FOUND INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                        160 CTACAGGGATCCTCAGGCACCCACTGCGAG 189
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ilarity 100.0%;
Conservative (
                              (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     9.3%; Score 30;
100.0%; Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 24;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 30;
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ABK52208
ID ABK
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                                                                                                                                                                                                                                                                                                                 Query Match
                                                               irrigation water; waste stream; contaminated aqueous medium; biological fluid; gastrointestinal tract; chelon protein; enteric bacteria; toxic metal ion; mercury; cadmium; divalent cation;
                  WO200230962-A2.
                                         Synthetic
                                                             heavy metal
                                                                                                 Mercuric ion; contaminated soil; ground water; hydroponic solution;
                                                                                                                      Synthetic product 1 forward PCR primer for construction of pASK-MBD
                                                                                                                                                                                          ABK52208 standard; DNA; 33 BP
                                                                                                                                                                                                                                                                                                                                  Sequence 568 BP; 130 A; 150 C; 164 G; 124 T; 0 other;
                                                                                                                                                13-AUG-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                        The mercury resistance genes can be used as selectable markers when used to transform other bacteria.
                                                                                                                                                                                                                                                                                                                                                                                        Claim 1; Page 2; 26pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                                                              Thiobacillus sp.
                                                                                                                                                                                                                                                                                                                                                                                                                    Mercury resistant control gene merR and shuttle vector - for enhanced expression of mercury resistance marker in transformed
                                                                                                                                                                                                                                                                                                                                                                                                                                                          P-PSDB; AAR49668
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1994-077131/10.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    11-JAN-1994.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (DOWA ) DOWA MINING CO LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Thiobacillus ferrooxidans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Resistance; mercury; selectable marker; Thiobacillus ferrooxidans;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mercury resistant control gene merR(1).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              -10_signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       transformation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  35_signal
                                                                                                                                                                                                                                                                                                      Local Similarity
                                                                                                                                                                                                                                              383 AAGATGGCCGACTTGGCGCGCATGGA 408
                                                                                                                                                                                                                                                          61 AAGATGGCCGACTTGGCGCGCATGGA 86
                                                                                                                                                                                                                                                                                             26;
                                                        binding protein; pASK-MBD; PCR; primer; ss.
                                                                                                                                                                                                                                                                                           Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        91JP-0018338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            91JP-0018338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /*tag= 89..568
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /*tag=
76..79
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      detection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /*tag= a
46..51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /product= merR(1) gene product.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /*tag= d
                                                                                                                                                                                                                                                                                                  8.1%; Score 26; DB 15; 100.0%; Pred. No. 0.0009;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ъ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           O
                                                                                                                                                                                                                                                                                          0,
                                                                                                                                                                                                                                                                                          Mismatches
                                                                                                                                                                                                                                                                                                    0.0009;
                                                                                                                                                                                                                                                                                         0,
                                                                                                                                                                                                                                                                                                              Length 568;
                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                       Gaps
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0;

18-APR-2002

31-MAR-1996

(first entry)

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RESULT 7
ABK52209/c
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XEXTXEX
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                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Vibrio cholerae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Vibrio cholerae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Vibrio cholerae disrupted haemolysin gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   W09510300-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           cholera; toxin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       07-OCT-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 7076 BP; 1578 A; 1975 C; 1968 G; 1555 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               immunity and the mercury resistance gene allows the vaccine strain to be identified without the use of antibiotics. The new strains of not revert to the cholera toxin positive phenotype. For treatment approx. 1 million organisms are taken orally, in aqueous NaHCO3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        encoding mercury resistance and the cholera toxin B subunit are inserted into a haemolysin gene. Expression of the B subunit ensures that the new strains are immunogenic, inducing a strong local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        used in vaccines to protect against cholera caused by non-01 strains, optionally together with CVD111 which protects against 01 strains. The new strains are derived from the 0139 serotype and the DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Example 11; Figure 21; 109pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New avirulent strains of Vibrio cholerae expressing toxin B sub:unit - are stable against reversion and useful in oral vaccines to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WPI; 1995-161574/21.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Kaper JB,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (UYMA-) UNIV MARYLAND BALTIMORE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         08-OCT-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       08-OCT-1993;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  20-APR-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New avirulent Vibrio cholerae strains of a non-01 serogroup can be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  induce local protective immunity
           Synthetic product 1 reverse PCR primer for construction of pASK-MBD
                                            13-AUG-2002 (first entry)
                                                                           ABK52209;
                                                                                                        ABK52209 standard; DNA; 33 BP
                                                                                                                                                                                                                                                                                                                                                                                        Local Similarity
                                                                                                                                                                                                                                                  5667
                                                                                                                                                                                                                                                                                                             5607 CACTGCGAGGAGGCCAGCCTGGCCGAACACACACGTCAAGGACGTGCGCGAGAAAGATG 5666
                                                                                                                                                                                                                                                                               67
                                                                                                                                                                                                                                                                                                                                                                           161;
                                                                                                                                                                                                                                                                                                                                          7 CACTGCGAGGAGGCCAGCCTGGCCGAACACACAAGCTCAAGGACGTGCGCGAGAAGATG 66
                                                                                                                                                                                                                                                                 GCCGACTTGGCGCGCATGGAAACCGTGCTGTTCTGAACTCGTGTGCGCCTGCCATGCACGA 126
                                                                                                                                                                                                               AAGGGGAATGTTTCCTGCCCGTTGATCGCGTCACTACAGGG 167
                                                                                                                                                                                                                                                GCCGACTTGGCGCGCATGGAAACCGTGCTGTCTGAACTCGTGTGCGCCTGCCATGCACGA 5726
                                                                                                                                                                                    Levine MM;
                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          93US-0133438
93US-0133439
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ; avirulent; serogroup; immunogenic; vaccine; mercury resistance; cholera toxin B subunit; ss.
                                                                                                                                                                                                                                                                                                                                                                         50.2%; Score 161; DB 16; Length 7076; 100.0%; Pred. No. 3e-74; tive 0; Mismatches 0; Indels 0.
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Matches Query Match

33;

Conservative

100.0%; Pieu. 100.0%; Pieu. +ive 0; Mismatches

10.3%;

Score 33;

DB 24; 2.1e-07;

Length 33; Indels

0;

Gaps

0;

Local Similarity

ABK52210 Ħ RESULT 8

ABK52210 standard; DNA; 30 BP

EXTXXX

13-AUG-2002 (first entry)

Synthetic product 2 forward PCR primer for construction of pASK-MBD

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Mercuric ion; contaminated soil; ground water; hydroponic solution; irrigation water; waste stream; contaminated aqueous medium; biological fluid; gastrointestinal tract; chelon protein; enteric bacteria; toxic metal ion; mercury; cadmium; divalent cation; heavy metal binding protein; pASK-MBD; PCR; primer; ss.
                                           metal ions from contaminated soil, ground water, hydroponic solutions or irrigation water of waste streams. The DNA of the invention, when immobilised onto a solid support, is useful for concentrating heavy metal ions from contaminated environment waste streams or contaminated on seedium including biological fluids. The nucleic acid, when aqueous medium including biological fluids. The nucleic acid, when recombinantly expressed in enteric bacteria (which are nontoxigenic and nonpathogenic), is suitable for use in the in vivo sequestration and elimination of mercuric ion from gastrointestinal tracts of animals or humans exposed to toxic metal ions such as mercury and/or cadmium. The nucleic acid of the invention are also useful in water treatment resins. The nucleic acid of the invention is highly specific and binds divalent cation such as mercury or cadmium with high affinity. The present nucleic acid sequence represents synthetic product 1 reverse PCR primer that was used in the methods of the invention for construction of pask-MBD vector.
                                                                                                                                                                                                                                                                                                                                                                                                        recombinant DNA molecule comprising a sequence encoding a chelon protein which binds mercuric ions. The invention is useful for recombinantly producing a protein in a host-cell, by infecting or transforming a host cell capable of expressing a chelon coding sequence with a vector comprising a promoter active in the host cell operably linked to a coding region for the protein to produce a recombinant host cell and culturing the recombinant host cell under conditions, where DNA is expressed. The nucleic acid encoding the chelon protein is useful for binding divalent mercuric ions, to take up, sequester and concentrate the heavy divalent mercuric ions, to take up, sequester and concentrate the heavy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel non-naturally occurring recombinant DNA molecule encoding a chelon protein useful for binding divalent cation mercury from contaminated soil, water, aqueous medium including biological fluids -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2002-435437/46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12-OCT-2000; 2000US-240465P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12-OCT-2001; 2001WO-US31819.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention relates to a new non-naturally occurring
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Page 24; 42pp; English.
Sequence 33 BP; 7 A; 9 C; 11 G; 6 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Caguiat JJ;
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RESULT 5
AAQ20186
             PX PX AX
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                                                                                                                                                                                                                                                                                                                  Ωy
                                                                                                                                                                                                                                                                                                                                                                                                                    cell capable of expressing a chelon coding sequence with a vector comprising a promoter active in the host cell operably linked to a coding term for the protein to produce a recombinant host cell under conditions, where DNA is expressed. CC the recombinant host cell under conditions, where DNA is expressed. CC divalent mercuric ions, to take up, sequester and concentrate the heavy cell integration water of waste streams. The DNA of the invention, when cell intrigation water of waste streams. The DNA of the invention, when cell cans from contaminated environment waste streams or contaminated environment waste streams or contaminated environment waste streams or contaminated cell intrigation of mercuric ion from gastrointestinal tracts of animals or nonpathogenic), is suitable for use in the in vivo sequestration and cell call of the invention are also useful in water treatment resins. CC molecules of the invention are also useful in water treatment resins. CC acido such as mercury or cadmium with high affinity. The present nucleic acid sequence encodes the Shigella flexneri wild-type Merk protein of the invention. This sequence was used in the methods of the invention for the protein of the invention of the methods of the invention for the protein of the invention of the methods of the invention for the protein of the invention of heavy metal binding proteins termed chelons.
                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                               Matches 161; Conservative
      HlyA gene with ctxB and mer gene inserted
                                       31-MAR-1992
                                                                     AAQ20186;
                                                                                            AAQ20186 standard; DNA; 7076 BP
                                                                                                                                                                                                                                                                                                                                                                                              Sequence 435 BP; 95 A; 113 C; 146 G; 81 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              which binds mercuric ions. The invention is useful for recombinantly producing a protein in a host cell, by infecting or transforming a host
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel non-naturally occurring recombinant DNA molecule encoding a chelon protein useful for binding divalent cation mercury from contaminated soil, water, aqueous medium including biological fluids -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        recombinant DNA molecule comprising a sequence encoding a chelon protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention relates to a new non-naturally occurring
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Page 20; 42pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2002-435437/46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12-OCT-2000; 2000US-240465P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (UYGE-) UNIV GEORGIA RES FOUND INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12-OCT-2001; 2001WO-US31819
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18-APR-2002.
                                                                                                                                                                                          127 AAGGGGAATGTTTCCTGCCCGTTGATCGCGTCACTACAGGG 167
                                                                                                                                                                       361
                                                                                                                                                                                                                              301
                                                                                                                                                                                                                                                                           241 CACTGCGAGGAGGCCAGCAGCCTGGCCGAACACAAGCTCAAGGACGTGCGCGAGAAGATG 300
                                                                                                                                                                                                                  7
                                                                                                                                                               AAGGGGAATGTTTCCTGCCCGTTGATCGCGTCACTACAGGG 401
                                                                                                                                                                                                                                                                                                        CACTGCGAGGAGGCCAGCAGCCTGGCCGAACACAAGCTCAAGGACGTGCGCGAGAAGATG 66
                                   (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Caguiat JJ;
                                                                                                                                                                                                                                                                                                                                                     50.2%; Score 161; DB 24; Length 435; 100.0%; Pred. No. 3.2e-74;
                                                                                                                                                                                                                                                                                                                                          0; Mismatches
                                                                                                                                                                                                                                                                                                                                          Indels
                                                                                                                                                                                                                                                                                                                                         0;
                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                            QΥ
                                                                                                                                                                                                                                                                                                                                    AAQ86906
                                                                                                                                                         DЪ
                                                                                                                                                                                  ρy
                                                                                                                                                                                                                  Вb
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                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                                                                                    Query Match
AAQ86906;
                        AAQ86906 standard; DNA; 7076 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               05-JUN-1991;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Vibrio cholerae.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12-DEC-1991.
                                                                                                                                                                                                                                                                                       Local Similarity
                                                                                                                                                                                                                                                                      161;
                                                                                                                                                                                     67
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Sequence 7076 BP; 1578 A; 1978 C; 1966 G; 1554 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The sequence is that of the haemolysin (hlyA) gene with two genes inserted into it, the cholera toxin subunit B gene (ctxB) and a mercury resistance gene (mer). It is used in the creation of a Vibrio cholerae strain that has have 100% efficacy in protecting humans against subsequent infection with a strain of a similar serotype and avoid undesirable side effects such as diarrhoea, nausea and cramping. Cultures of these strains may be used for prodn. of vaccines against cholera. It is unclear whether the mer gene sequence is that of the sense or anti-sense strand as neither appears to have a clear reading frame. See also AAQ20185.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Fig 21; 83pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New Vibrio cholerae strains - comprise restriction endonuclease fragment encoding toxin, used as vaccines against cholera
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Kaper JB, Baudry-Maurelli B,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (UYMA-) UNIV MARYLAND BALTI.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Cholera; vaccine; enterotoxin; diarrhoea; ss.
5667 GCCGACTTGGCGCGCATGGAAACCGTGCTGTCTGAACTCGTGTGCGCCTGCCATGCACGA 5726
                                                                                                                                                                                                                          5607 CACTGCGAGGAGGCCAGCAGCCTGGCCGAACACAAGCTCAAGGACGTGCGCGAGAAGATG 5666
                                                                                                                                                                                                                                                                                7 CACTGCGAGGAGGCCAGCAGCCTGGCCGAACACACAAGCTCAAGGACGTGCGCGAGAAGATG 66
                                                                                                                                            GCCGACTTGGCGCGCATGGAAACCGTGCTGTTCTGAACTCGTGTGCGCCTGCCATGCACGA 126
                                                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             91WO-US03812.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5882..7076
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "resumption of hlyA gene"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /*tag= c
/note= "inserted mer gene"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      5873..1602
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 'note= "inserted ctxB gene"
                                                                                                                                                                                                                                                                                                                                                                          100.0%;
                                                                                                                                                                                                                                                                                                                                                                    50.2%; Score 161; DB 13; Length 7076; 100.0%; Pred. No. 3e-74;
                                                                                                                                                                                                                                                                                                                                                  0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fasano A;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Mercuric ion; contaminated soil; ground water; hydroponic solution; irrigation water; waste stream; contaminated aqueous medium; biological fluid; gastrointestinal tract; chelon protein; enteric bacteria; toxic metal ion; mercury; cadmium; divalent cation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Adjacent plasmid region encoding variant MerR protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13-AUG-2002 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABK52213;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ABK52213 standard; DNA; 509 BP.
The present invention relates to a new non-naturally occurring recombinant DNA molecule comprising a sequence encoding a chelon protein which binds mercuric ions. The invention is useful for recombinantly producing a protein in a host-cell, by infecting or transforming a host cell capable of expressing a chelon coding sequence with a vector comprising a promoter active in the host cell operably linked to a coding region for the protein to produce a recombinant host cell and culturing the recombinant host cell under conditions, where DNA is expressed.
                                                                                                                                                                                                                                                                                                                                                                                                                                           18-APR-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WO200230962-A2.
                                                                                                                                                                                     Novel non-naturally occurring recombinant DNA molecule encoding a chelon protein useful for binding divalent cation mercury from contaminated soil, water, aqueous medium including biological fluids
                                                                                                                                                                                                                                                                                                                                                                            12-OCT-2000; 2000US-240465P.
                                                                                                                                                                                                                                                                                                                                                                                                            12-OCT-2001; 2001WO-US31819
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        heavy metal binding protein; MerR;
                                                                                                                                                           Disclosure; Page 25; 42pp; English.
                                                                                                                                                                                                                                                         P-PSDB; AAU97552.
                                                                                                                                                                                                                                                                                                            Summers AO,
                                                                                                                                                                                                                                                                                                                                           (UYGE-) UNIV GEORGIA RES FOUND INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            301
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CACTGCGAGGAGGCCAGCAGCCTGGCCGAACACAAGCTCAAGGACGTGCGCGAGAAGATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAGATGGCCGACTTGGCGCGCATGGAAACCGTGCTGTCTGAACTCGTGTGCGCCTGCCAT 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GCCGACTTGGCGCGCATGGAAACCGTGCTGTTCTGAACTCGTGTGCGCCTGCCATGCACGA 300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GCACGAAAGGGGAATGTTTCCTGCCCGTTGATCGCGTCACTACAGGGATCCTCAGGCACC 180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAGATGGCCGACTTGGCGCGCATGGAAACCGTGCTGTCTGAACTCGTGTGCGCCTGCCAT 120
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                                                                                                                                                                                                                                                                                                            Caguiat JJ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /product=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /*tag=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              "Variant MerR protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             gene; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  240
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CC The nucleic acid encoding the chelon protein is useful for binding CC divalent mercuric ions, to take up, sequester and concentrate the heavy CC metal ions from contaminated soil, ground water, hydroponic solutions or CC irrigation water of waste streams. The DNA of the invention, when CC immobilised onto a solid support, is useful for concentrating heavy metal CC cons from contaminated environment waste streams or contaminated CC recombinantly expressed in enteric bacteria (which are nontoxigenic and CC nonpathogenic), is suitable for use in the in vivo sequestration and CC elimination of mercuric ion from gastrointestinal tracts of animals or CC humans exposed to toxic metal ions such as mercury and/or cadmium. The nucleic acid of the invention are also useful in water treatment resins. CC molecules of the invention are also useful in water treatment resins. CC cation such as mercury or cadmium with highly specific and binds divalent CC acid represents the adjacent plasmid region that encodes the variant Merr CC protein of the invention.
                                                                                                                                                                                                                                                                                                                                                                                     ABK52206
ID ABK5
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Matches 321;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 509 BP; 139 A; 128 C; 140 G; 102 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                       ABK52206 standard; DNA; 435 BP
                                                                                                                                                                                          Mercuric ion; contaminated soil; ground water; hydroponic solution; irrigation water; waste stream; contaminated aqueous medium; biological fluid; gastrointestinal tract; chelon protein; enteric bacteria; toxic metal ion; mercury; cadmium; divalent cation;
                                                                                                                                                                                                                                                                                DNA encoding Shigella flexneri wild-type MerR protein.
                                                                                                                                                                                                                                                                                                                     13-AUG-2002
                                                                                                                                                                                                                                                                                                                                                         ABK52206;
                                                                                                                                       Shigella flexneri.
                                                                                                                                                                          heavy metal binding protein; MerR; gene; ds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 241 GCCGACTTGGCGCGCATGGAAACCGTGCTGTCTGAACTCGTGTGCGCCTGCCATGCACGA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 181 CACTGCGAGGAGGCCAGCCTGGCCGAACACAAGCTCAAGGACGTGCGCGAGAAGATG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Conservative
                                                                                                                                                                                                                                                                                                                     (first entry)
                                                     /product= "Shigella flexneri wild-type MerR protein"
                                                                                                        Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                100.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0
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WO200230962-A2

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CC producing a protein in a host-cell, by infecting or transforming a host cell capable of expressing a chelon coding sequence with a vector comprising a promoter active in the host cell operably linked to a coding region for the protein to produce a recombinant host cell and culturing the recombinant host cell under conditions, where DNA is expressed.

CC The nucleic acid encoding the chelon protein is useful for binding cometal ions from contaminated soil, ground water, hydroponic solutions or immobilised onto a solid support, is useful for concentrate the heavy compatible of the invention water of waste streams. The DNA of the invention, when concentrating heavy metal ions from contaminated environment waste streams or contaminated concentrating heavy metal constrainment is useful for concentrating heavy metal constrainment protein and concentrating heavy metal constrainment waste streams or contaminated concentration and concentration of mercuric ion from gastrointestinal tracts of animals or molecules of the invention are also useful in water treatment resists. Concentration acid of the invention is highly specific and binds divalent acid sequence encodes the synthetic Merr chelon variant protein of the concentration of the invention. This sequence encodes one of the heavy metal binding proteins
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 321;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 321 BP; 72 A; 94 C; 103 G; 52 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present invention relates to a new non-naturally occurring recombinant DNA molecule comprising a sequence encoding a chelon protein which binds mercuric ions. The invention is useful for recombinantly
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Disclosure; Page 21; 42pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    contaminated soil, water, aqueous medium including biological fluids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel non-naturally occurring recombinant DNA molecule encoding a chelon protein useful for binding divident cation mercury from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Summers AO,
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                                                                                                                                                                                                                                                                                                                                                                                                  61 AAGATGGCCGACTTGGCGCGCATGGAAACCGTGCTGTCTGAACTCGTGTGCGCCTGCCAT 120
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                          GCCGACTTGGCGCGCATGGAAACCGTGCTGTCTGAACTCGTGTGCGCCTGCCATGCACGA 300
                                                                                                                                                                                                   CACTGCGAGGAGGCCAGCAGCTGGCCGAACACACAGCTCCAAGGACGTGCGCGCGAGAAGATG
                                                                                                                                                                                                                                                                   AAGGGGAATGTTTCCTGCCCG 321
                                            AAGGGGAATGTTTCCTGCCCG 321
                                                                                                                                                                      CACTGCGAGGAGGCCAGCCTGGCCGAACACAAGCTCAAGGACGTGCGCGAGAAGATG
                                                                                                                                                                                                                                                                                                             GCACGAAAAGGGGAATGTTTCCTGCCCGTTGATCGCGTCACTACAGGGATCCTCAGGCACC
                                                                              AAGATGGCCGACTTGGCGCGCATGGAAACCGTGCTGTCTGAACTCGTGTGCGCCTGCCAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATGACACACTGCGAGGAGGCCAGCAGCCTGGCCGAACACAAGCTCAAGGACGTGCGCGAG 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATGACACACTGCGAGGAGGCCAGCAGCCTGGCCGAACACAAGCTCAAGGACGTGCGCGAG 60
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%; Score 321; DB 24
100.0%; Pred. No. 1e-157;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 24; Length 321;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0,
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1 ATGACACACTGCGAGGAGGCCAGCCAGCCTGGCCGAACACAAGCTCAAGGACGTGCGCGAG 60 Matches Query Match

Local

Similarity

100.0%; Score 321; DB 24 100.0%; Pred. No. 1e-157;

DB 24; Length 354;

Conservative

0;

Mismatches

0

Indels

0;

Gaps

60

Sequence 354 BP; 83 A; 103 C; 111 G; 57 T; 0 other;

Qy В

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cc recombinant DNA molecule comprising a sequence encoding a chelon protein combinant DNA molecule comprising a sequence encoding a chelon protein combinantly protein in a host-cell, by infecting or transforming a host cell capable of expressing a chelon coding sequence with a vector comprising a promoter active in the host cell operably linked to a coding region for the protein to produce a recombinant host cell and culturing the recombinant host cell operably linked to a coding the recombinant host cell under conditions, where DNA is expressed. Cc divalent mercuric ions, to take up, sequester and concentrate the heavy irrigation water of waste streams. The DNA of the invention, when climated into a solid support, is useful for concentrating heavy metal consistent mercuric ions from contaminated environment waste streams or contaminated conto a solid support, is useful for concentrating heavy metal aqueous medium including biological fluids. The nucleic acid, when conspathogenic), is suitable for use in the in vivo sequestration and climatation of mercuric ion from gastrointestinal tracts of animals or conteminant of the invention are also useful in water treatment resins. The nucleic acid of the invention as mercury and/or cadmium. The contents exposed to toxic metal ions such as mercury and/or cadmium. The cation such as mercury or cadmium with high affinity. The present nucleic acid sequence represents the bASK-MBD gene. as described in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ABK52212
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Novel non-naturally occurring recombinant DNA molecule encoding a chelon protein useful for binding divalent cation mercury from contaminated soil, water, aqueous medium including biological fluids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention relates to a new non-naturally occurring
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; Page 24; 42pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 2002-435437/46
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (UYGE-) UNIV GEORGIA RES FOUND INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12-OCT-2001; 2001WO-US31819
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mercuric ion; contaminated soil; ground water; hydroponic solution; irrigation water; waste stream; contaminated aqueous medium; biological fluid; gastrointestinal tract; chelon protein; enteric bacteria; toxic metal ion; mercury; cadmium; divalent cation; heavy metal binding protein; PCR; pASK-MBD; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12-OCT-2000; 2000US-240465P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA encoding pask-MBD gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ABK52212;
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                                              sequence represents the pASK-MBD gene, as described in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Caguiat JJ;
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Run on:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Title:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Word size :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Post-processing: Listing first 45 summaries
                                                                                                                                                                                                                                                     Result
                                           a
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                                                                                                                                                                                                                                                                                                                                          pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                               Score
321
321
321
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161
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33
30
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321
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Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIDS2/gcgdata/geneseq/geneseqn-embl/NA199.DAT:*
/SIDS2/gcgdata/geneseq/geneseqn-embl/NA199.DAT:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1985.DAT:*
/SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1985.DAT:*
/SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1987.DAT:*
/SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1988.DAT:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1981.DAT:*/SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1982.DAT:*/SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1983.DAT:*/SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1984.DAT:*/SIDS2/gcgdata/geneseq/geneseqn-emb1/NA1984.DAT:*
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                                                                                                                                                                                                                                                                                                                                                                                                                                      /SIDS2/gcgdata/geneseq/geneseqn-embl/NA2001A.DAT:*
/SIDS2/gcgdata/geneseq/geneseqn-embl/NA2001B.DAT:*
/SIDS2/gcgdata/geneseq/geneseqn-embl/NA2002.DAT:*
                                                                                                                                                                                                                                    Length
                                                                      7076
7076
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ABK52209
ABK52210
AAQ58554
                                                                      AAQ20186
AAQ86906
                                                                                                                                          ABK52212
ABK52213
                                                                                                                    ABK52206
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RESULT 1
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                                                                                                                                                                                                                                               DNA encoding synthetic MerR chelon variant.
                                                                                                                                                                                                                                                                                             ABK52207;
                                                                                                                                                                                                                                                                                                                 ABK52207 standard; DNA; 321 BP.
                                                                                                                                                              Synthetic.
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12-OCT-2001; 2001WO-US31819.

18-APR-2002. WO200230962-A2

/product= "Synthetic MerR chelon variant"
/product= "This sequence encodes the first 107 amino acids
/note= "This sequence encodes the first 107 amino acids
of the synthetic MerR chelon variant. This
sequence lacks a stop codon"

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Database :
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REFERENCE AUTHORS TITLE

JOURNAL

1 Summers,A.O. and Caguiat,J.J. Metal binding proteins, recombinant host cells and methods Patent: WO 0230962-A 3 18-APR-2002; UNIVERSITY OF GEORGIA RESEARCH FOUNDATION, INC. (US) score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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128 c 140 g
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/db_xref="taxon:32630"
/note="sequence encoding chelon
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RESULT 4 AX473150 LOCUS

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AX473150 435 bp Sequence 1 from Patent WO0230962.

linear

PAT 09-AUG-2002

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                                                                                                                                                                                                                                    Direct Submission
Submitted (18-DEC-2001) Kholodii G.Y., Russian Academy of Sciences, Submitted of Molecular Genetics, Kurchatov Sq. 2, Moscow 123182,
                                                                                                                                                                                                                                                                                                                                                                 bacteria
                                                                                                                                                                                                                                                                                                                                                                                  Kholodii,G.Y., Gorlenko,Z.M., Mindlin,S.Z. and Nikiforov,V.G. Distribution of distinct microvariants of Tn5041 in environments
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AJ422224.1 GI:19848211 merR gene; MerR protein.
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                                                                                                                                                                                                                                                                                                             Kholodii, G.Y.
                                                                                                                                                                                                                                                                                                                                                  Unpublished
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                                                                                                                                                                                                                     sequence Y09209
                                            /note="isolated from mercury mine, ore"
                                                               /country="Kyrgyzstan:Khaidarkan"
                                                                                                   /sex="Tra+ (narrow range)"
                                                                                                                         /db_xref="taxon:294"
                                                                                                                                              /strain="KHP22"
                                                                                                                                                       /organism="Pseudomonas fluorescens"
               transposon="Tn5041G"
                                                                                        /plasmid="pKHP22"
                                                                                                                                                                                              Location/Qualifiers
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/db_xref="taxon:623"
/note="To21 of plasmid R100"
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                                                                                                                                                                                                        Direct Submission
                                                                                                                                                                                                                                                                                Kholodii,G.Y., Gorlenko,Z.M., Mindlin,S.Z. and Nikiforov,V.G. Distribution of distinct microvariants of Tn5041 in environmental
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445 bp DNA linear BCT 07-JUL-200
Pseudomonas fluorescens (strain KHP25) transposon Tn5041G, partial
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/transl_table=11
/product="MerR protein"
a 149 c 119 g 8
                                                                                        /organism="Pseudomonas fluorescens"
/strain="KHP25"
        /country="Kyrgyzstan:Khaidarkan"
/note="isolated from mercury mine, ore"
                                          /sex="Tra+ (narrow range)"
/plasmid="pKLH22"
                                                                          /db_xref="taxon:294"
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of insertion of the Tn21 homologue"
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/transposon="Tn21deltaIn2"
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-35_signal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         263 CACTGCGAGGAGGCCAGCAGCCTGGCCGAACACCAAGCTCAAGGACGTGCGCGAGAAGAGTG
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                                                                                                                                                                                                                                                                                                                                                            merR; regulatory protein.
Alcaligenes faecalis.
Alcaligenes faecalis
                                                                                                                                                                                                                                                                                                                                                                                                                                                             ARMERGE4 516 bp DNA linear BCT A.faecalis (SE20MERR) merR gene for regulatory protein.
                                                                                                                                    Submitted (13-MAY-1994) Osborn A. M., University of Li
Genetics and Microbiology, Liverpool, Merseyside, UK,
                                                                                                                                                                                                                                                                    Osborn,A.M., Bruce,K.D., Strike,P. and Ritchie,D.A. Sequence Conservation between Regulatory Mercury Resistance Genes
                                                                                                                                                                                                                                                                                                                                                                                                                        Z33484.1 GI:607038
                                                                                                                                                                                                                            Unpublished
                                                                                                                                                                                                                                                                                                                                              Bacteria; Proteobacteria; beta subdivision; Alcaligenaceae;
                                                                                                                                                                        Direct Submission
                                                                                                                                                                                                                                                  from Mercury Polluted and Pristine Environments
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /transposon="In5041G"
31. .35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="Merr protein"
/protein_id="CaD19592.1"
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/db_xref="GI:19848213"
/translation="VETIREYQRKGLLPEPDKPYGSIRRYGEADVVRVKFVKSAQRLG
/translation="VETIRESSLAEHKLKDVREKMADLARMETVLSELVCACHARKG
FSLDEIAELLRLDGGTHCEEASSLAEHKLKDVREKMADLARMETVLSELVCACHARKG
NVSCPLIASLQGEAGLARSAMP"
149 c 119 g 89 t
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of insertion of the Tn21 homologue"
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/transposon="Tn21deltaIn2"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /function="activator/repressor"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  rpt_type-INVERTED
  /clone="pSE20R1, pSE20R2"
complement(13. .18)
                                                        /organism="Alcaligenes faecalis"
/isolate="SE20"
                                                                                                              Location/Qualifiers
                                                                                                                                                                                                            1 to 516)
                                          db_xref="taxon:511"
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                                                                                                                                                          University of Liverpool,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              7 CACTGCGAGGAGGCCAGCAGCCTGGCCGAACACAAGCTCAAGGACGTGCGCGAGAAGATG
                                                                                                                                                                                                                                                                                                                              1 (bases 1 to 3763)
Barrineau, P., Gilbert, P., Jackson, W.J., Jones, C.S., Summers, A.O. and Wisdom, S.
provided by A.O. Summers, 15-SEP-1986. Potential Shine-Dalgarno provided by A.O. Summers, 15-SEP-1986. Potential Shine-Dalgarno sequences are located at positions 157-162 (13.1 kd), 590-596 (12.4 kd), 1740-1745 (59 kd) and 545-542 (15.9 kd). A single 38 bp inverted repeat, which delimits the leftward end of Tn21, Tn4 and Tn501 extends from nucleotide 65-102. A promoter region for the structural genes is located between positions 366-585. This area contains regions of dyad symmetry which might function as operator sites for merk, which negatively regulates the expression of the structural genes as well as its own expression.
                                                                                                                                                                                                                                                                                                                                                                                                    merA gene; merR gene; merT gene; mercuric reducta plasmid NR1 (IncFII) from E.coli DNA, clone pDB7. Plasmid NR1
                                                                                                                                                                                                                                                                                               The DNA sequence of the mercury resistance operon of the IncFII plasmid {\tt NR1}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NRIMER Plasmid NRI mercury resistance (mer) operon.
                                                                                                                                                                             Summers, A.O.
Unpublished (1986)
[2] revises [1].
                                                                                                                                                                                                                                                                                                                                                                                                                                                         K03089.1 GI:150389
                                                                                                                                                                                                                                                    6530603
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Rygeadyvrvkfyksaorlgfsldeiaellrlddgthceeasslaehklkdvrekmad
Larmefylselvcacharkgnvscpllaslogbegglarsamp"
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/protein_id="CAA83892.1"
/db_xref="GI:607039"
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/transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                          mercuric reductase
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FEATURES
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                                                                                                                                                                                                                                                          /protein_id="aab59077.1"
/db_xref="G1:150395"
/tabslation="MGLMTRIADKTGALGSVVSAMGCAACFPALASFGAAIGLGFLSQ
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NLMYVGLALMIGVSIWDFVSPAHRRCGPDGCELPAKRL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /transi_table=11
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/db_xref="GC:150394"
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                           /translation="mSTLKITGMTCDSCAVHVKDALEKVPGVQSADVSYAKGSAKLAIEVGTSPDALTAAVAGLGYRATLADAASVSTPGGLLDKMRDLLGRNDKTGSSGALHIAV
                                                                                        /transl_table=11
/protein_id="AAB59078.1"
/db_xref="GI:150396"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /transl_table=11
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/protein_id="AB59074.1"
/db_xref="GI:150392"
/translation="MRAKSAIFSRTSLSLCSARLLASSQWVPSSSRNSSAISSRLNPS
IGSGGAAMAAALKAVEQGARVTLIERGTIGGTCVNVGCVPSKIMIRAAHIAHLRRESP
                                                                                                                                                                                 codon_start=1
                                                                                                                                                                                                         /note="Hg(II) reductase (59.0 kd merA)"
                                                                                                                                                                                                                                                                                                                                                                                                                /transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="15.0 kd merTC protein"
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/db_xref="GI:150393"
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RLGKNANGQVFQIIFHIA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /protein_id="AAB59073.1"
/db_xref="GI:150391"
/translation="MAGAHEFROHGFHARQVGHLLAHVLELVFGOAAGLLAVGAIVEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /db_xref="GI:455296"
/tbanslation="MENNLENLTIGVFAKAAGVNVETIRFYQRKGLLREPDKPYGSIR
/translation="MENNLENLTIGVFAKAAGVNVETIRFYQRKGLLREPDKPYGSIR
RYGEADVVRVKFYKSAQRLGFSLDEIAELLRLDDGTHCEEASSLAEHKLKDVREKMAD
LARMETYLSELVCACHARKGNVSCPLIASLQGEAGLARSAMP"
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/note="15.9 kd merR protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           232 GCCGACTTGGCGCGCATGGAAACCGTGCTGTCTGAACTCGTGTGCGCCTGCCATGCACGA 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         292 CACTGCGAGGAGGCCAGCCTGGCCGAACACAAGCTCAAGGACGTGCGCGAGAAGATG
85014891
6091128
                         Misra,T.K., Brown,N.L., Fritzinger,D.C., Pridmore,R.D., Barnes,W.M., Haberstroh,L. and Silver,S.
Mercuric ion-resistance operons of plasmid R100 and transposon Tn501: the beginning of the operon including the regulatory region and the first two structural genes
Proc. Natl. Acad. Sci. U.S.A. 81 (19), 5975-5979 (1984)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  67 GCCGACTTGGCGCGCATGGAAACCGTGCTGTTCTGAACTCGTGTGGGCCCTGCCATGCACGA 126
                                                                                                                                                                6265806
3 (bas
                                                                                                                                                                                                                             Ohtsubo,H., Nyman,K., Doroszkiewicz,W. and Ohtsubo,E. Multiple copies of iso-insertion sequences of IS1 in Shigella dysenteriae chromosome
                                                                                                                                                                                                                                                                                                                                                     Ohtsubo, H. and Ohtsubo, E. Nucleotide sequence of an insertion element, I Proc. Natl. Acad. Sci. U.S.A. 75 (2), 615-619
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R1004 STATE DNA linear BCT 01-OF Plasmid R100 putative (insA), putative (insB), merR (merR), putative (merT), merC (merC), mercuric reductase (merA), and
                                                                                                                                                                                                                  Nature 292 (5824), 640-643 (1981)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           IS1 insertion sequence; merC gene; merR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                         (bases 849 to 2189)
                                                                                                                                                                                                                                                                                                    (sites)
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/replace=""
696 a 1198 c 1189 g
bp upstream of EcoRII site.
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IYOLANDGGERVVAFDRCLIAPGACSPAVPPIPGLKDTPYWTSTEALVSETIPKRLAVIG
SSVVALELAQAFARLGAKVTINLARSTLFFREDPAIGEAVTAAFRÆGIEVREHTQASQ
VAXINGEGDGEFVLTTAHGELRADKLLVATGRAPNTRKLALDATGVTLTPGGAIVIDP
GMRTSVEHIYAAGDCTDQPQFVYVAAAAGTRAAINMTGGDAALNLTAMFAVVFTDPQV
ATVGTSEAEAHHDGIKTDSRTLTLDMVPRALANFDTRGFIKLVVEEGSGRLIGVQAVA
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/replace=""
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; Pred. No. 2.9e-71;
; amatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Mercuric reductase structural genes from plasmid R100 and transposon Tn501: functional domains of the enzyme Gene 34 (2-3), 253-262 (1985)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cause loss of translocation activity.

Three R100 derived small circular plasmids (pSM1, pSM2, pSM5)

Three R100 derived small circular pSM2 consists of map units 82.7-89.3 (the 3' end of contain ISIR, pSM2 consists of map units 87.4-88.6. pSM 15 consists of map units 87.4-88.6. pSM 15 consists of map units
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Brown, N.L., Misra, T.K., Winnie, J.N., Schmidt, A., Lien, C., Sieff, M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Silver, S.
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Misra,T.K., Brown,N.L., Haberstroh,L., Schmidt,A., Goddette,D. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          83.4-89.3 in circularized form.

Potential -35 regions are found at positions 980-984 and 1402-1406 and -10 regions at positions 999-1006 and 1425-1431. Unidentified reading frames are found at positions 2143-2565, 4688-4924 (gtg start codon), and 4921 to 5593. [4] noted two other ORF's in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished
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[2] sites; insA and insB spans.
cocation/Qualifiers
1. 5747
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929. .966
                                                                                                                                                                                                                                                                                                                                                                                /gene="in: 478. .855
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  /gene="merR"
1080. .1262
                                                       1080.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="putative"
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                                                                              /note="Tn21 inverted repeat"
                                                                                                                                                                                                                                                                                                                        note="putative"
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GMRTSYEHIYAAGDCTDQPQFYYVAAAAGTRAAINMTGGDAALNLTAMPAVVFTDPQV
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/translation="MSEPQNGRGALFAGGLAAILASTCCLGPLVLVALGFSGAWIGNL
TVLEPYRPLFIGAALVALFFAWKRIYRPVQACKPGEVCAIPQVRATYKLIFWIVAVLV
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4329. .4691
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skyegyskydygfekreavvtfddtkasvgkltkatadagypssvkg"
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            The nucleotide sequence of the mercuric resistance operons of plasmid R100 and transposon Tn501: further evidence for mer gawhich enhance the activity of the mercuric ion detoxification
                                                                                         Brown, N.L., Misra, T.K., Winnie, J.N., Schmidt, A.,
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Cell 42 (2), 629-638 (1985)
                                                                                                                                                                                                               tnpM: a novel regulatory gene that enhances Tn21 transposition and
                                                                                                                                                                                                                                             6 (bases 3057 to 4105)
Hyde, D.R. and Tu, C.P.
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Rogowsky,P., Halford,S.E. and Schmitt,R.
Definition of three resolvase binding sites at the res loci of Tn21
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The DNA sequence of the mercury resistance operon of the IncFII
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Recchia,G.D., Stokes,H.W. and Hall,R.M.
Characterisation of specific and secondary recombination sites recognised by the integron DNA integrase
Nucleic Acids Res. 22 (11), 2071-2078 (1994)
                                                                                                                              Gene 142 (1),
94237488
                                                                                                                                               Levesque,C., Brassard,S., Lapointe,J. and Roy,P.H. Diversity and relative strength of tandem promoters for the antibiotic-resistance genes of several integrons Gene 142 (1), 49-54 (1994)
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Allmeler, H., Cresnar, B., Greck, M. and Schmitt, R.
Complete nucleotide sequence of Tn1721: gene organization and
novel gene product with features of a chemotaxis protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mercier, J., Lachapelle, J., Couture, F., Lafond, M., Vezina, Boissinot, M. and Levesque, R.C.
Structural and functional characterization of tnpI, a reclocus in Tn2l and related beta-lactamase transposons
J. Bacteriol. 172 (7), 3745-3757 (1990)
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Guerineau,F., Brooks,L. and Mullineaux,P.
Expression of the sulfonamide resistance gene from plasmid R46
Plasmid 23 (1), 35-41 (1990)
90272799
                                                                                                                                                                                                                                                                                                                            Untwist and shout: a heavy metal-responsive transcriptional
                                                                                 17 (bases 4492 to 8992)
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                                                                                                                                                                                                                                                                                                               regulator
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A novel family of potentially mobile DNA elements encoding site-specific gene-integration functions: integrons Mol. Microbiol. 3 (12), 1669-1683 (1989) 90158115
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         10 (bases 5384 to 5397; 6199 to 6253) Schmidt,F.R., Nucken,E.J. and Henschke,R.B. Structure and function of hot spots providing site-directed specific recombination and gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sundstrom, L., Radstrom, P., Swedberg, G. and Skold, O.
Site-specific recombination promotes linkage between trimethoprim-
and sulfonamide resistance genes. Sequence characterization of
dhfrv and sull and a recombination active locus of Tn21
Mol. Gen. Genet. 213 (2-3), 191-201 (1988)
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Mol. Gen.
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Ward, E. and Grinsted, J.
The nucleotide sequence of the tnpA gene of
Nucleic Acids Res. 15 (4), 1799-1806 (1987)
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J. Bacteriol. 176 (11), 3257-3268 (1994)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Recchia,G.D. and Hall,R.M.

Gene cassettes: a new class of mobile element
Microbiology 141 (Pt 12), 3015-3027 (1995)
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                                                                                                                          27 (bases 7540 to Hall, R.M. Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Collis,C.M., Kim,M.J., Stokes,H.W. and Hall,R.M. Binding of the purified integron DNA integrase Intl1 to integron- and cassette-associated recombination sites Mol. Microbiol. 29 (2), 477-490 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21 (bases 9951 to 14934)
Brown, H.J., Stokes, H.W. and Hall
The integrons In0, In2, and In5
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                                                                                                                                                              GenBank Accession
27 (bases 7540 +>
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Partridge,S.R. and Hall,R.M.
In34, a complex In5-like class 1 integron containing orf513 and
                                                                                                                                                                                                                                                                                                                                                                                          Liebert, C.A., Hall, R.M. and Summers, A.O. Transposon Tn21, flagship of the floating genome Microbiol. Mol. Biol. Rev. 63 (3), 507-522 (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18 (bases 4048 to 4159; 14945 to 15031)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nucleic Acids Res. 26 (19), 4347-4355 (1998)
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                                                                                                                                                                                                                                             26 (bases 4106
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                                                                                 Similarity
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                                                                   Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Submitted (20-SEP-1999) National Chung Hsing University, Institute of Molecular Biology, 250 Kuo Kuang Road, Taichung, Taiwan,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Chen, J.-H. and Chen, J.-Y.
TnSF1, a Tn21-like transposon
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                                                                                                                                                                                                                                   /product="putative transposase"
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/protein_id="AAG14402.1"
/db_xref="Gi:10185690"
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/translation="MpRRSILSAAERESILALPDSKDDLIRHYTENDTDLSIIRQRRG
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HLSELQTVFGFFRPTWSHYRQAVQMLTELAMOTDKGIVLASALIGHLRRQSVLLPALN
AVERASAEAITRANRRIYDALAEPLADAHRRLLDLLKRRDGNGKTTWLAWLRQSPAKP
NSRHMLEBITERLKANQALDLPTGIERLVHQNRLLKIAREGGQMTPADLAKFEPORRYA
AVERASAEAITAANQALDLPTGIERLVHQNRLLKIAREGGQMTPADLAKFEPORRYA
NTLVALATEGMATVTDEIIDLHDRILGKLFNAAKNKHQQQFQASGKAINAKVRLYGRIG
QALIDAKQSGRDAFAAIEAVASWDSFARSVTBAQKLAQPDDFDFLHRIGESYATLRY
APEFLAVLKLRAAPAAKNVLDAIEVLRGMNTDNARKLPADAFTGTIKFWGKLVMTDA
GIDRRYYELCALSELKNSLRSGDIWVQGSRQFKDFEDYLVPPEKFTSLKQSSELPLAV
ATDCGQYLHERUTILLENQLATVNRMAAANDLDDAITESCLKITPLDAAVPDTAQALI
DQTAMVLPHYKITELLLEVDEWTGFTRHFTHLKSGDLAKDKNLLLTTILADAINGCTONO
DGTAMVLPHYKITELLLEVDEWTGFTRHFTHLKSGDLAKDKNLLLTTILADAINGCTONO
DGTAMVLPHYKITENCIATURDFTWVGTBIAVVNAOEBBUDDAACHDGTONGCTCON
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/strain="SH595"
/db_xref="taxon:623"
/transposon="TnSF1"
/note="Tn21-like"
                                                                                                                                       KMAESC PGTTYAKLAWLQAWHTRDETYSTALAELVNAQFRHPPAGHWGDGTTSSSDGO
NERTASKAKSTGHINPKYGSSPGRTFYTHISDQYAPFHTKVNNVGLDSTYVLDGLLY
HESDLRIEBHYDDTAGFTDHVFALMHLLGFRFAPRIRDLDGTKLYIPKGDAXIDAKDA
MIGGTLNIKHVRAHWDEILRLATSIKQGTVTASLMLRKLGSYPRQNGLAVALRELGRI
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                                                      KIGAGKFRPLRPLQPA"
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                                                                                                          ERTLF ILDWLQSVELRRRVHAGLNKGEARNALARAVF FNRLGE IRDRSF EQQRYRASG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="tnpA"
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/gene="tnpR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /transl_table=11
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                               .3563)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GPAASHPDARPVSPADEIRRIAPLLDALSDQMHRVSIDSFQPETQRYALKRGVGYLND
IQGFPDPALYPDIAEADCRLVVMHSAQRDGIATRTGHLRPKDALDEIVRRFEERVSAL
RRSGVAADRLILDPGMGFFMSPAPETSLHVLSNLQKLKSALGLPLLVSVSRKSFLGAT
                                                                                                                                                                                                                                                          /codon_start=1
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/gene="mphA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="dihydropteroate synthase"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       {\tt VGLPVKDLGPASLAAELHAIGNGADYVRTHAPGDLRSAITFSETLAKFRSRDARDRGL}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     IRFHGVRHPATLGSSEVEAFLSWLANERKVSVSTHRQALAALLFEYGKVLCTDLPWLQ
EIGRPRPSRRLPVVLTPDEVVRILGFLEGEHRLFAQLLYGTGWRISEGLQLRVKDLDF
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KYPRAGHSWPWFWVFAQHTHSTDPRSGVVRRHHMYDQTFQRAFKRAVEQAGITKPATP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /function="may confer resistance to erythromycin"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="mphA"
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/gene="sull"
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7600. .8439
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LEALISFARTGDTVVVHSMDRLARNILDDLRRIVQTLTQRGVHIEFVKEHLSFTGEDSP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26485 GCCGACTTGGCGCGCATGGAAACCGTGCTGTCTGAACTCGTGTGCGCCTGCCATGCACGA 26544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  127 AAGGGGAATGTTTCCTGCCCGTTGATCGCGTCACTACAGGG 167
Submitted (18-MAY 1999) Gen-ichi Sampei, The University of Electro-Communications, Department of Applied Physics and Chemistry; 1-5-1, Chofugaoka, Chofu, Tokyo 182-8585, Japan (E-mail:sampei@pc.uec.ac.jp, Tel:81-424-43-5492,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     67 GCCGACTTGGCGCGCATGGAAACCGTGCTGTCTGAACTCGTGTGCGCCTGCCATGCACGA 126
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 merR; merT; merC; merA; merD; yadA; yaeA; tniA; tniBdeltal; yahA; istA; istB; ybbA; sull; qacEdeltal; aadAl; intR; tnpM; tnpR; yahA; ybtA; cat; insA; insB; ycdA; ycdB; stbB; stbB; stbA; ycgA; ycgB; ychA; yciB; ycjA; ycjB; ydaA; ydbB; ydcA; yddA; ysgB; ydeA; ydjA; ydjA; ydjB; yeaA; tetR; tetC; tetD; yedA; yefA; psiB; psiA; mok; hok; yeeA; yetA; 32; X; traW; finP; traJ; traY; traB; traB; traB; traB; traY; yfA; traD; traY; tr
                                                                                                                                                                                                                                                Unpublished
2 (bases 1
                                                                                                                                                              Sampei, G. and Mizobuchi, K. Direct Submission
                                                                                                                                                                                                                                                                                                                                 Organization and diversification of plasmid
                                                                                                                                                                                                                                                                                                    nucleotide sequence of the R100 genome
                                                                                                                                                                                                                                                                                                                                                                          Sampei, G. and Mizobuchi, K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sprasmids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Plasmid R100
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AP000342.1 GI:5103148
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7506 c 7633 g
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DRWEPELNEAIPNDERDTTMPAAMATTLRKLLTGELLTLASRQQLIDWMEADKVAGPL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="bla"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement (21228.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                50.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         7633 g
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              94281 bp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product-"regulatory protein of mer operon"
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/protein_id="BAA78785.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /lab host="Escherichia coli strain K-12"
/note="Plasmid R100 is also referred to as NR1 or R222"
join(59. .7369,11456. .19730)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement(92. .526)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement (92. .526)
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/db_xref="taxon:28399"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /codon_start=1
/transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /gene="merR"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ocation/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TVLEPYRPLFIGAALVALFFAWKRIYRPVQACKPGEVCAIPQVRATYKLIFWIVAVLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /transl_table=11
/product="mercuric transport protein"
/protein_id="BAA78786.1"
/db_xref="GI:5103150"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="100% identical to gp:NRIMER_1[MerR of plasmid NR1]"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           organism="Plasmid R100"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /translation="mkklfaslalaaavapvmaatQtvtlavpgmtcaacpttvkkal
skvegvskydvgfekreavvtfddtkasvQkltkatadagvpssvkQ"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note="100% identical to gp:NRIMER_4[MerT of plasmid NR1]"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                {\tt LARMETVLSELVCACHARKGNVSCPLIASLQGEAGLARSAMP}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          transposon="Tn21"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product="mercuric transport protein"
/protein_id="BAA78787.1"
/db_xref="GI:5103151"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="100% identical to gp:NRIMER_5[MerP of plasmid NR1]"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LVALGFPYVVPFFY"
                                                                                                                                                                                                            SFGAAIGLGFLSQYEGLFISRLLPLFAALAFLANALGWFSHRQWLRSLLGMIGPAIVF
AATJWLLCNWWTANLMYVGLALMIGVSIWDFVSPAHRRCGPDGCELPAKRL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       codon_start=i
                                                                                                                                                                                                                                                                                        /product="mercuric transport protein"
/protein_id="BAA78788.1"
/db_xref="GI:5103152"
                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="merC"
1234. .1695
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        codon_start=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="merP"
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/protein_id="BAA78789.1"
                                               /transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                         note="100% identical to gp:NRIMER_6[MerC of plasmid NRI]"
                                                                                             note="100% identical to gp:R1004_6[MerA of plasmid R100]"
                                                                                                                                                                                                                                                                 translation="MSQQANDNSESRFMGLMTRIADKTGALGSVVSAMGCAACFPALA
                                                                                                                                                                                                                                                                                                                                                            transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                     codon_start=1
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/translation="mstlkitgmtcdscavhykdalekvpgvqsadvsyakgsaklai
/translation="mstlkitgmtcdscavhykdalekvpgvqsadvsyakgsskalhiav
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fdgglaltptiqrtallaqqqarvdelrhakyegilekgnpaltylhagsarkdurri
pygtlndegervartclatggaspavppipglkdtpymtstealvsetipkrlavig
ssyvalelaqafarlgakvtilarstlffredpalgeavtaafrwegievrehtqasq
yayingegdgefylttaheelradkllvatgrapntrklaldatgytltpqgalvidp
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ATVGYSEAEAHHDGIKTDSRTLTLDNVPRALANFDTRGFIKLVVEEGSGRLIGVQAVA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /protein_id="BAA78790.1"
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AALQRLCFVRAAFEAGIGLDALARLCRALDAADGAQAAAQLAVLRQLVERRRAALAHL
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/gene="merD"
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                                                                                                                                                                                                                                                                                                                                                                                                                                4833. .6512
/gene="tniA"
4833. .6512
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PEAGELIQTAALAIRNRMTVQELADQLFPYLTMVEGLKLAAQTFNKDVKQLSCCAG"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /translation="MTSSQPAGWTAAELAQAAARGQLDLHYQPLVDLRDHRIAGAEAL WARWRHERLGLLEPGQFTLPLAESFGLWPEIGAWVLGEACROMHKWGCEPAWQPFKLAINV ASASQVGPTFDDEVKRVLADMALPAELLEIELTESVAFGNPALFASEDALRAIGVFFPA DDFGTGYSCLQHLKCCFJTTLKIDQSFVARLPDDARDQTIVRAVIQLAHGLGMDVIFR RRLHQLIGRNGCGAASS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /translation="mnapdklppetropvsgylwgalavltcpchlpilaavlagtta
gaflgehwgyaalaltglfvlavtrllrafrggs"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DAQLASMPAERAHEEALP"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       gene product of plasmid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                join(4692. .7369,11456. .15691)
/transposon="In2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /codon_start=1
/transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="yaeA"
/note="99% identical to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /protein_id="BAA78791.1"
/db_xref="GI:5103155"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             note="100% identical to gp:ECOMERTET_3[urf1, putative RF, gene product of plasmid R100]"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       'gene-"yadA"
NKAALTLRELERWLTLAVGTYHGSVHNGLLQPPAARWAEAVARVGVPAVVTRATSFLV
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MVVTLEAPSAVSVGLCLVHVACDKRPWLEGLNVENDWQMSGKPLLLYLDNAAEFKSEA
                                                                                                                      QKRFLTKQKRSLAAFHREVTQVCKAQKLRVPARNTVALRIASLDPRKVIRRREGQDAA
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/db_xref="GI:5103156"
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admaaqalglsrrqyyvlirrarqgsslytdlypgqssggkgkgklpepyervihell
                                                                                                                                                                                                         /product="transposase of In21"
/protein_id="BAA78793.1"
/db_xref="GI:5103157"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="yaeA"
                                   LRRGCEQHGIRLDYRPLGQPHYGGIVERIIGTAMQMIHDELPGTTFSNPDQRGDYDSE
                                                                                                                                                                                                                                                                                                      transl_table=11
                                                                                                                                                                                                                                                                                                                                         /codon_start=
                                                                                                                                                                                                                                                                                                                                                                                                'gene="tniA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      note="terminal IR of In2"
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R100]"
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COMMENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CCC
                                                                                                                                                                                    JOURNAL
                                                                    JOURNAL
                                                                                                                  AUTHORS
                                                                                                                                                                                                                               TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ORGANISM
                                                                                                                                                                                                                                                                                                                                                                                                                   AUTHORS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                127 AAGGGGAATGTTTCCTGCCCGTTGATCGCGTCACTACAGGG 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           226 GCCGACTTGGCGCGCATGGAAACCGTGCTGTCTGAACTCGTGTGCGCCTGCCATGCACGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Parkhill, J., Dougan, G., James, K.D., Thomson, N.R., Pickard, D., Wain, J., Churcher, C., Mungall, K.L., Bentley, S.D., Holden, M.T.G., Sebaihia, M., Baker, S., Basham, D., Brooks, K., Chillingworth, T., Connerton, P., Cronin, A., Davis, P., Davies, R.M., Dowd, L., White, N., Farrar, J., Feltwell, T., Hamlin, N., Haque, A., Hien, T.T., Holroyd, S., Jagels, K., Krogh, A., Larsen, T.S., Leather, S., Moule, S., O'Gaora, P., Parry, C., Quail, M., Rutherford, K., Simmonds, M., Skelton, J., Stevens, K., Whitehead, S. and Barrell, B.G. Complete genome sequence of a multiple drug resistant Salmonella Mature 413 (6858), 848-852 (2001)
Direct Submission
Submitted (25-OCT-2001) Submitted on behalf of the Salmonalla sequencing team, Sanger Centre, Wellcome Trust Genome Campus, Hinxton, Cambridge CB10 1SA E-mail: parkhill@sanger.ac.uk
                                                                                                        Parkhill, J
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Salmonella enterica subsp. enterica serovar Typhi. Salmonella enterica subsp. enterica serovar Typhi
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AL513383.1 GI:16505740
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Plasmid pHCM1
AL513383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Salmonella enterica serovar Typhi (Salmonella typhi) strain CT18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            7 CACTGCGAGGAGGCCAGCCTGGCCGAACACAAGCTCAAGGACGTGCGCGAGAAGATG 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                             Salmonella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STYPPHCM1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GCCGACTTGGCGCGCATGGAAACCGTGCTGTTCTGAACTCGTGTGCGCCTGCCCATGCACGA 126
                                                                                                                                (bases 1 to 218160)
                                                                                                                                                                                                                                                                                                                                                                                                                                  (bases 1 to 218160)
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7370. .7395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ALNRLEALYAWPNKORWPNILLLVGPTNNGKSMIVEKFRRTHPASSDADQEHIPVLVVQ
MPSEPSVIRTYVALLAAMGAPLRPRPRLPEMEQLALALLRKVGVRMLVIDELHNVLAG
NSVNRREFLNLLRFLGNELRIPLVGVGTRDAYLAIRSDDQLENRFEPMMLPVWEANDD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="NTP-binding protein"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CCSLLASFAASLPLRRPSPIATLDMARYLLTRSEGTIGELAHLLMAAAIVAVESGEEA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    INHRTLSMAC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="100% identical to gp:TTU42226_7 [TniBdeltal of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATRKARRDADRRQHLKTSARPDKPVPPDTDIADPQADNLPPAKPFDQIEEW"
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GQHYLEIPYRTLSHPAVTLWEQRQALAKLRQQGREQVDESALFRWIGQMREIVTSAQK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /transl
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/gene="tniBdeltal"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /codon_start=1
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Pred. No. 1.8e-71;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             218160 bp
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Details of S. typhi sequencing at the Sanger Centre are available on the World Wide Web.
/note="HCM1.04c, insB, possible IS1 transposase, len: 156 aa; highly similar to many from Enterobacteriaceae e.g. SW:ISB_ECOLI (EMBL:D10483), insB, Escherichia coli insertion element IS1 protein InsB (167 aa), fasta scores, E(): 0, 91.6% identity in 167 aa overlap"
                                                                                                                                    /note="HCM1.04c" complement(1876. .2346) /gene="insB"
                                                                                                                                                                                                            complement(1876, .2346)
/gene="insB"
                                                                                                                                                                                                                                                                                                       complement(1871. .2585)
/note="IS1"
                                                                                                                                                                                                                                             /note="13 bp_inverted_repeat flanking IS1"
                                                                                                                                                                                                                                                                                                                                                   /note="possible RBS"
                                                                                                                                                                                                                                                                                                                                                                                                                   /translation="mnkplysfaelsgnainvarqsvidmemdatrekigkarslfhs
gihravngypliqsaanqlavikrllgdtkyldacitenlcmfspegylylfmqrrfi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        , where "HUM1.03c, hypothetical protein, len: 107 aa; unknown function"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /transl_table=11
/product="hypothetical protein"
/protein_id="CAD109620_1"
/db_xref="GI:16505742"
/translation="MMYPDITGVKMKLSQLEVGMTVWSLSRTKMGNTTIKTVTLHSVV
                                                                                                                                                                                                                                                                                                                                                                          complement(1697.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product="hypothetical protein"
/protein_id="CAD09621.1"
/db_xref="GI:16505743"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement(1367. .1690)
/gene="HCM1.03c"
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/gene="HCM1.02c"
complement(742. .1053)
/gene="HCM1.02c"
/note="HCM1.02c"
/note="HCM1.02c, hypothetical protein, len: 103 aa;
unknown function"
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/note="possible RBS"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  transl_table=11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         codon_start=]
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /translation="mnotetgpsgftettvdeeriairvmigdvvgryrkovppdrvq
katfevnggllmalllallmlvciiqrlatgdrlmsftgepdvrdiqftlmlviefal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         {\tt KEVHDNHVIASWNGNAPRRFGETAITGWKKEKPLLIRDRSGSARLATREEKARILDT}
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /product="putative membrane protein"
/protein_id="CAD09619.1"
/db_xref="GI:16505741"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     complement(1, .528)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /gene="HCM1.01c"
complement(1..528)
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Typhi"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /transl_table=11
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /plasmid-"pHCM1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /db_xref="taxon:90370"
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/protein_id="cad09622.1"
/db_xref="GI:16505744"
/db_xref="GI:16505744"
/translation="megnrehygrwpohdftsfkklrposvtsriopgsdvivcaksr
/translation="megnrehygrwpohdftsfkklrposvtsriopgsdvivcaksr
ORWLFYAYDRLRKTVVAHVFGERTMATLGRKSLSFSKSVELHDKVIGHYLNIKHYQ"
LHVISKRYTQRIEHHLNLRQHLARLGRKSLSFSKSVELHDKVIGHYLNIKHYQ"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="HCM1.05c, insA, probable IS1 transposase, len: 91 aa; highly similar to many from Enterobacteriaceae e.g. sw:ISA1_ECOLI (EMBL:X52534), insA, Escherichia coli insertion element IS1 protein InsA (91 aa), fasta scores; E(): 0, 98.98 identity in 91 aa overlap. Contains PS00017 amp/GTP-binding site motif A (P-loop). Contains probable helix-turn-helix motif at aa 67-88"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="ps00017 ATP/GTP-binding site motif A (P-loop)"
complement(2573. .2585)
/note="13 bp inverted repeat flanking IS1"
complement(2694. .3644)
/gene="corA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product-"putative IS1 transposase"
/protein_id="0AD09623.1"
/db_xref-"G1:16505745"
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/TASDPCTHQKIIDMAMNGYGCRATARIMGVGLNTILRHLKNSGRSR"
YTASQPCTHQKIIDMAMNGYGCRATARIMGVGLNTILRHLKNSGRSR"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="HCM1.07c, corA, probable magnesium and cobalt transport protein, len: 316 aa; similar to many e.g. SW:CORA_ECOLI (EMBL:L11042), corA, Escherichia coli magnesium and cobalt transport protein (316 aa), fasta scores; E(): 0, 99.1% identity in 316 aa overlap. Contains pramatch to entry PF01544 CorA, CorA-like Mg2+ transporter protein. Contains hydrophobic, possible membrane-spanning regions"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note-"possible translational frameshift site, similar to that determined experimentally (EMBL:X52534)" complement(2472. .2495)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 complement(2265.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       codon_start=1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement(2694. .3644)
/gene="corA"
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                                                                                                                                                                                                                                                                                                                                                               ELGQSLATRPELEDIEASARFEDDOGLHIHSFFFFEDAEDHAGNSTVAFTIRDGRLF
TLRERELPAERLYRMARSQSMYDGNAYELLLDLFETKIEQLADEIENIYSDLEQLSR
VIMEGHQGDEYDEALSTLAELEDIGWKVRLCLMDTQRALNFLYRKARLPGGQLEQARE
ILRDIESLLPHNESLFQKVNFLMQAAMGFINIEQNRIIKIFSVYSVVFLPPTLVASSY
                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product="putative magnesium and cobalt transport protein" /protein_id="CAD09624.1" /db_xref="GI:16505746" /db_xref="GI:16505746" /translation="MLSAFQLENNRLTRLEVEESOPLVNAVWIDLVEPDDDERLRLQS
                                                                                                                                                                                                          transporter protein, sc
complement(3653. .3656)
                                                                                                                                                                                                                                                                                                               complement(2697. .3584)
                                                                                                                                                                                                                                                                                                                                          GMNFEFMPELKWRFGYPAAIIFMILAGLAPYLYFKRKNWL"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /codon_start=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /transl_table=11
/gene="HCM1.08"
/note="HCM1.08, hypothetical protein, len: 109 aa;
                                                                           'gene="HCM1.08"
                                                                                                                                                                                                                                   note="Pfam match to entry PF01544 CorA, CorA-like Mg2+
transporter protein, score 432.90, E-value 2.8e-126"
                                                                                                      ="possible RBS"
.4343
                                                                                                                                                                                  possible RBS"
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Query Match
Best Local :
                -10_signal
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 175250 AAGGGGAATGTTTCCTGCCCGTTGATCGCGTCACTACAGGG 175290
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         127 AAGGGGAATGTTTCCTGCCCGTTGATCGCGTCACTACAGGG 167
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  161;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              K.oxytoca (SE31MERR) merR gene for regulatory protein
                                                                                                                                                                                                                                                                                                                                                Osborn,A.M., Bruce,K.D., Strike,P. and Ritchie,D.A. Sequence Conservation between Regulatory Mercury Resistance Genes from Mercury Polluted and Pristine Environments
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Klebsiella oxytoca.
Klebsiella oxytoca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    merR gene; regulatory protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Z33485.1 GI:607036
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AFMERGE5
                                                                                                                                                                                                                    Submitted (13-MAY-1994) Osborn A. M., University of Liverpool Genetics and Microbiology, Liverpool, Merseyside, UK, L69 3BX
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
                                                                                                                                                                                                                                                                   Direct Submission
                                                                                                                                                                                                                                                                                   Osborn, A.M.
                                                                                                                                                                                                                                                                                                                               Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                             Klebsiella
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/protein_id="cAD09625.1"
/protein_id="cAD09625.1"
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/tanslation="MAHQLLIGKGMITLNLKRIFLALTLLPLFAVAADDCALSDPTLT
/translation="MAHQLLIGKGMITLNLKRIFLALTLLPLFAVAADDCALSDPTLT
VQAYTVNPQTERVKMYWQKANGEAWGTLHALLADINSQGQYQMAMNGGILNLTVFDIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  to the N-terminal half of SW:YIGE_ECOLI (EMBL:L02122), yigE, Escherichia coli hypothetical protein (254 aa), fasta scores; E(): 0, 97.9% identity in 95 aa overlap"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                complement(4363. .4569)
/gene="HCM1.10c"
/note="HCM1.10c, hypothetical protein, len: 68 aa; unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement(4363. .4569)
/gene="HCM1.10c"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /product-"hypothetical protein"
/protein_id="CAD09626.1"
/db_xref="GI:16505748"
/translation="MGHYDYTRTLRYQLYDASRFHDGATAEQAGELHTVAFSKPAIAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Y XXXXXXX
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/trans1_table=11
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                                                               /clone="pSE31R1, pSE31R2, pSE31R3" complement(13. .18)
                     complement(28.
                                                                                                                                                     /organism="Klebsiella oxytoca"
                                          /citation=[1
                                                                                                         /db_xref="taxon:571"
                                                                                                                                                                                               Location/Qualifiers
/citation=[1]
                                                                                                                                /isolate="SE31"
                                                                                                                                                                                                                                                                                                          1 to 537)
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 Mismatches

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AUTHORS
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ECU77087/c
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (01-NOV-1996) Microbiology, University of Georgia, 527 Biological Sciences, Athens, GA 30602-2605, USA
                                                                                                                                                                                                                                                                                                     Direct Submission
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Escherichia.

1 (bases 1 to 1696)

Ogawa, H. I., Tolle, C.L. and Summers, A.O.

Physical and genetic map of the organomercury resistance (Omr) and inorganic mercury resistance (Hgr) loci of the IncM plasmid R831b gene 32 (3), 311-320 (1984)
                                                                                                                                                                                                                                                                                                                 Liebert, C.A., Watson, A.L. and Summers, A.O.
                                                                                                                                                                                                                                                                                                                                                               Nucleotide sequence of the organomercury resistance (OMR) locus Unpublished (1996)
                                                                                                                                                                                                                                                                                                                                                                                                    Tolle, C., Totis, P. and Summers, A.O.
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Escherichia coli
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                                                                                         complement(1. .305)
/note="similar to GenBank Accession Numbers M24940 and U60777; partial 5' tnpA gene and tnpA promoter region"
                                                                                                                                                           /organism="Escherichia coli"
/db_xref="taxon:562"
/plasmid="R831b"
                                               complement(306. .740)
                                                                                   complement(306. .740)
/note="similar to GenBank Accession Number M24940; mer
                               /gene="merR"
                                                                      /gene="merR"
                                                                                                                                                                                                                                             Location/Qualifiers
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RYGEADVTRYFYKSAGRAGESLDEIAELLRLEDGTHCEEASGLAEHKLKDVREKMAD
LARMEAVLSELVCACHARKGRVSCPLLASLQDGTKLAASARGSHGVTMP"
136 c 175 g 116 t
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/protein_id="CAA83893.1"
/db_xref="GI:607037"
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72. .527
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                                                                                                                   175 GGCACCCACTGCGAGGAGGCCAGCAGCCTGGCCGA 209
                                                                          506 GGCACCCACTGCGAGGAGGCCAGCAGCCTGGCCGA 472
                                                                                                                                                                       35;
                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                             '(translation="MKLAPYILELLTSVNRTNGTADLLVPLLRELAKGRPVSRTTLAG
ILDWPAERVAAVLEQATSTEYDKDGNIIGYGLTLRETSYVFELDDRRLYAWCALDTLI
EPALIGRPRAFVSSHCAATGAPVSLTVSPSEIQAVEPAGMAVSLVLPQEAADVRQSFCC
HVHFFASVPTAEDWASKHQGLEGLAIVSVHEAFGLGQEFNRHLLQTMSSRTP"

487 c 460 g 367 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note="similiar to merA sequence, GenBank Accession
Numbers M15049 and KO3089; truncated 3' nonfunctional end
of merA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="possible merB -10 signal site" complement(773. .778) /note="possible merR -10 signal site" complement(793. .798)
                                                                                                                                                                                                                                                                                                                                                                           /product="MerB"
/protein_id="AAB49639.1"
/db_xref="GI:1679731"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             organomercurial lyase"
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/transl_table=11
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/db.xref-"G1:1679730"
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/translation-"MENNLENLTIGVFAKAAGVNVETIRFYQRKGLLPEPDKPYGSIR
RYGAADVTRYKEVKSAQRLGFSLDETAELLRLDDGTHCEEASSLAEHKLQDVREKMAD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="similar to GenBank Accession Number M15049;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="merB"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               complement(793. .798)
/note="possible merR -35 signal site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="merB"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="18 base pair hyphenated dyad; MerR binding site;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          operon regulatory protein"
/codon_start=1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LARMEAVLSDLVCACHSRQGNVSCPLIASLQGGTSLAGASTA"
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                                                                                                                                                                                    10.9%; Score 35; 100.0%; Pred. No.
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